

Gencore version 5.1.6  
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Run on: February 20, 2004, 15:25:26 ; Search time 40.3032 Seconds  
(without alignments)  
2847.400 Million cell updates/sec

perfect score: 3884  
Sequence: 1 GSSIKIRUTVILCAKNLAKK..... EKLYEKULLTAVESTCGRAVE 723

Searched: 1107863 seqs, 158726573 residues

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

**Post-processing:** Minimum Match 0%  
Maximum Match 100%  
Listing first 45

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1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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4: /SIBS1/gcgdat

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6: /SIDS1/gcadata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS1/gcadata/geneseq/geneseq-emb1/AA1987.DAT:*
8: /SIDS1/gcadata/geneseq/geneseq-emb1/AA1987.DAT:*

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10: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1989.DAT*
11: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1990.DAT*
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13: /SIDSI1/gcadata/geneseq/geneseqP-emb1/AI1992.DAT *
14: /SIDSI1/gcadata/geneseq/geneseqP-emb1/AI1993.DAT *
15: /SIDSI1/gcadata/geneseq/geneseqP-emb1/AI1994.DAT *

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17: /SIDS1/gcadata/geneseq/geneseqp-emb1/A11996.DAT:*
18: /SIDS1/gcadata/geneseq/geneseqp-emb1/A11997.DAT:*
19: /SIDS1/gcadata/geneseq/geneseqp-emb1/A11998.DAT:*
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20: /SIDS1/gcgdata/geneseq/geneseq-p-emb1/AA2009.DAT;
21: /SIDS1/gcgdata/geneseq/geneseq-p-emb1/AA2009.DAT;
22: /SIDS1/gcgdata/geneseq/geneseq-p-emb1/AA2001.DAT; *
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Pred. No. is the number of results predicted by chance to have a value of 1.

Score greater than or equal to the score of the result being and is derived by analysis of the total score distribution

No.	Score	Match	Length	DB	ID	Description
1	3884	100.0	723	22	AAB31476	Amino acid sequenc
2	3878	99.8	722	24	AAB312724	B3 ubiquitin ligas
3	3869	99.6	722	24	AAM9851	Human protein SEQ
4	3001	77.3	748	18	AAM13384	Human protein ubiq
5	3001	77.3	748	22	ABR31477	Amino acid sequenc
6	2996	77.1	804	22	AASV96110	Human acidic diagnostic a
7	2236	57.6	514	22	AABU97301	Novel central nerv
8	2069	53.3	1035	22	ABB61120	Drosophila melanog
9	1644.5	41.6	335	22	AAM98877	Human protein SEQ

## ALIGNMENTS

## ALIGNMENTS

XX  
DT 20-APR-2001 (first entry)  
XX  
DE Amino acid sequence of a human Smurfl polypeptide..

**KX** Smurfl; Smurf2; Smad signal transduction; bone morphogenic protein; transforming growth factor-beta; human; TGF-beta; KX osteogenesis; blood differentiation; cartilage formation; neural tube patterning; retinal development; heart development; morphogenesis; tooth formation; gamete formation.

Score greater than or equal to the score of the result being prioritized and is derived by analysis of the total score distribution.



QY	62 VGGTDSITISVMHKKIHKGAGFGLCVRILSNAISRLKOTGYORLICKNPSDTAV	PR 03-FEB-2000; 2000US-0496914.
Db	61 VKTDTSITISVMHKKIHKGAGFGLCVRILSNAISRLKOTGYORLICKNPSDTAV	PR 27-APR-2000; 2000US-0566875.
QY	122 RGQIVSLQTRDRIGTGGSVDCRGLENEGTVDGSPGPRLSCMEEPAPYDSTGA 120	PR 20-JUN-2000; 2000US-059075.
Db	121 RGQIVSLQTRDRIGTGGSVDCRGLENEGTVDGSPGPRLSCMEEPAPYDSTGA 180	PR 19-JUL-2000; 2000US-0620325.
QY	182 AGGGCRVESPQDQLQARLNPDRGSIQTQNRPFRPHQSPRLPEPEGVQRTIVQQ 241	PR 01-SEP-2000; 2000US-0654936.
Db	181 AGGGCRVESPQDQLQARLNPDRGSIQTQNRPFRPHQSPRLPEPEGVQRTIVQQ 240	PR 15-SEP-2000; 2000US-0653561.
QY	242 VFLATQGVSTWDPRPRDLSVNCDLGPLPGLPQWEVRSVGRIVFHNRRTQFT 301	PR 20-OCT-2000; 2000US-0693325.
Db	241 VFLATQGVSTWDPRPRDLSVNCDLGPLPGLPQWEVRSVGRIVFHNRRTQFT 300	PR 30-NOV-2000; 2000US-0728422.
QY		XX (HYSE-) HISEQ INC.
Db		XX Tang YT, Liu C, Demanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
Db		XX PI Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
QY		XX PI AJ, Yang Y, Wehrman T, Goodrich R;
Db		XX DR WPI: 2001-476283/51.
QY		XX DR N-PSDB: AAK52994.
Db	302 DPLRHIMMHQCOLKEPSQPLPSEGSLDEBELPAQRYEDBLVKLKVHLRHSLOQQ 361	XX Nucleic acids encoding polypeptides with cytokine-like activities,
Db	301 DPRUHIMMHQCOLKEPSQPLPSEGSLDEBELPAQRYEDBLVKLKVHLRHSLOQQ 360	PT useful in diagnosis and gene therapy -
QY	362 AGHRIEVREEIFEESTRQIMKORPKDLKLMVKERGEGLDYGVAEWYLICHEM 421	XX
Db	361 AGHRIEVREEIFEESTRQIMKORPKDLKLMVKERGEGLDYGVAEWYLICHEM 420	CC The invention relates to polynucleotides (AAK51456-AAK5335) and the
QY	422 LNPYGLQYSTDMYMLQINPSSINDPLSYFHFGRLVAFHCHYNGGTFVPPY 481	CC encoded polypeptides (AAK78323-AAK8032) that exhibit activity elating to
Db	421 LNPYGLQYSTDMYMLQINPSSINDPLSYFHFGRLVAFHCHYNGGTFVPPY 480	CC cytokine, cell proliferation or cell differentiation or which may induce
QY	482 KOLSKPIQSUDSVEPDPLAKSVALENDTPVHTFCHEAHARGIQLHEKPKNGR 541	CC production of other cytokines in other cell populations. The
Db	481 KOLSKPIQSUDSVEPDPLAKSVALENDTPVHTFCHEAHARGIQLHEKPKNGR 540	CC polyimideptides are useful in gene therapy, vaccines or
QY	542 NVPVTEENKRYVRYANFRMRCIAEQLALQGFBELPQFLLAKPFDQKELLETTIGL 601	CC peptide therapy. The polypeptides have various cytokine-like activities,
Db	541 NVPVTEENKRYVRYANFRMRCIAEQLALQGFBELPQFLLAKPFDQKELLETTIGL 600	CC e.g. stem cell growth factor activity, haemopoiesis regulating
QY	602 DKIDLANDWKSNTTRKHCVAUDNTWFWQAVETDEERARLQFVGSTRVPLQFKAL 661	CC activity, tissue growth factor activity, immunomodulatory activity and
Db	601 DKIDLANDWKSNTTRKHCVAUDNTWFWQAVETDEERARLQFVGSTRVPLQFKAL 660	CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
QY	662 QGSTGAGPRLFTILIDANTDNLPAKAHTCFNRIDIPPYSESYEKLYERLTAVEETCGFA 721	CC inflammation.
Db	661 QGSTGAGPRLFTILIDANTDNLPAKAHTCFNRIDIPPYSESYEKLYERLTAVEETCGFA 720	CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK5282) and 3666
Db	722 VE 723	CC (AAW80220) are omitted as the relevant pages from the sequence listing
Db	721 VE 722	CC were missing at the time of publication.
RESULT 3		XX
ID AAM79861	Query Match 99.6%; Score 3869; DB 22; Length 722;	Sequence 722 AA:
AC AAM79861;	Best Local Similarity 99.9%; Pred. No. 0;	
XX	Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
XX	DB	
XX	QY	2 GSSIKIRTVLCAKNLAKDFPRLPDPFPEAKTVDDSGQHQHSTDVTKNTDPKNNQHYDLY 61
XX	DB	1 GSSIKIRTVLCAKNLAKDFPRLPDPFPEAKTVDDSGQHQHSTDVTKNTDPKNNQHYDLY 60
QY	62 VGGTDSITISVMHKKIHKGAGFGLCVRILSNAISRLKOTGYORLICKNPSDTAV 121	DB
Db	61 VKTDTSITISVMHKKIHKGAGFGLCVRILSNAISRLKOTGYORLICKNPSDTAV	QY
QY	122 RGQIVSLQTRDRIGTGGSVDCRGLENEGTVDGSPGPRLSCMEEPAPYDSTGA 180	Db 121 RGQIVSLQTRDRIGTGGSVDCRGLENEGTVDGSPGPRLSCMEEPAPYDSTGA 180
Db	182 AGGGCRVESPQDQLQARLNPDRGSIQTQNRPFRPHQSPRLPEPEGVQRTIVQQ 241	QY 182 AGGGCRVESPQDQLQARLNPDRGSIQTQNRPFRPHQSPRLPEPEGVQRTIVQQ 240
Db	181 AGGGCRVESPQDQLQARLNPDRGSIQTQNRPFRPHQSPRLPEPEGVQRTIVQQ 240	QY 181 AGGGCRVESPQDQLQARLNPDRGSIQTQNRPFRPHQSPRLPEPEGVQRTIVQQ 240
QY	242 VFLATQGVSTWDPRPRDLSVNCDLGPLPGLPQWEVRSVGRIVFHNRRTQFT 301	Db 242 VFLATQGVSTWDPRPRDLSVNCDLGPLPGLPQWEVRSVGRIVFHNRRTQFT 300
Db	241 VFLATQGVSTWDPRPRDLSVNCDLGPLPGLPQWEVRSVGRIVFHNRRTQFT 300	QY 241 VFLATQGVSTWDPRPRDLSVNCDLGPLPGLPQWEVRSVGRIVFHNRRTQFT 300
Db	302 DPRUHIMMHQCOLKEPSQPLPSEGSLDEBELPAQRYEDBLVKLKVHLRHSLOQQ 361	QY 302 DPRUHIMMHQCOLKEPSQPLPSEGSLDEBELPAQRYEDBLVKLKVHLRHSLOQQ 361
Db	301 DPRUHIMMHQCOLKEPSQPLPSEGSLDEBELPAQRYEDBLVKLKVHLRHSLOQQ 360	QY 301 DPRUHIMMHQCOLKEPSQPLPSEGSLDEBELPAQRYEDBLVKLKVHLRHSLOQQ 360
QY	362 AGHRIEVREEIFEESTRQIMKORPKDLKLMVKERGEGLDYGVAEWYLICHEM 421	QY 362 AGHRIEVREEIFEESTRQIMKORPKDLKLMVKERGEGLDYGVAEWYLICHEM 420
Db	361 AGHRIEVREEIFEESTRQIMKORPKDLKLMVKERGEGLDYGVAEWYLICHEM 420	QY 361 AGHRIEVREEIFEESTRQIMKORPKDLKLMVKERGEGLDYGVAEWYLICHEM 420
QY	422 LNPYGLQYSTDMYMLQINPSSINDPLSYFHFGRLVAFHCHYNGGTFVPPY 481	QY 422 LNPYGLQYSTDMYMLQINPSSINDPLSYFHFGRLVAFHCHYNGGTFVPPY 481

SQ	Sequence	748 AA;
Query	Match	77.3%; Score 3001; DB 18; Length 748;
Db	Best Local Similarity	74.6%; Pred. No. 6 4e-286; Matches 565; Conservative 63; Mismatches 71; Indels 58; Gaps 8;
Qy	Matches	565; Conservative 63; Mismatches 71; Indels 58; Gaps 8;
Db	541 KQJLGPPIQLSLESTDPEHLHSWLVLENDITPUDHTCVERHAGLQLQHLKPNR 541	
Qy	542 NVVTEENKEKTYRLYNNWRFGRLAQFLALQKGNELIPOHLIKPDKQEKLIGL 601	
Db	541 NVVTEENKEKTYRLYNNWRFGRLAQFLALQKGNELIPOHLIKPDKQEKLIGL 600	
Qy	542 NVVTEENKEKTYRLYNNWRFGRLAQFLALQKGNELIPOHLIKPDKQEKLIGL 600	
Db	562 DKJDNDWSNRFLKHCVADSHIVRPMQATEFDEBERRARLLQFTGTRVPGFCAL 661	
Qy	601 DKJDNDWSNRFLKHCVADSHIVRPMQATEFDEBERRARLLQFTGTRVPGFCAL 660	
Db	662 QGSTGAAGRRLFLTHLDANTNLPKAHTCNRIDIPPYESYEKLYKULTAVETCTFA 721	
Qy	661 QGSTGAAGRRLFLTHLDANTNLPKAHTCNRIDIPPYESYEKLYKULTAVETCTFA 720	
Db	721 VE 723	
Db	721 VE 722	
RESULT 4		
AAW13384		
ID	AAM13384 standard; Protein; 748 AA.	
XX		
AC	AAW13384;	
XX		
DT	10-JUL-1997 (first entry)	
DE	Human protein ubiquitin ligase publ.	
XX		
KW	Protein ubiquitin ligase; publ; cdc25 phosphatase; CDK kinase; p53; cell cycle; transgenic animal.	
KW	Homo sapiens.	
OS		
XX		
PN	W09712962-A1	
PD	10-APR-1997	
XX		
PF	04-OCT-1996; 96WO-US15930.	
XX		
PR	04-OCT-1995; 95US5-0539205.	
XX		
PA	(COLD-) COLD SPRING HARBOR LAB.	
XX		
PT	Beach, D., Caligiuri, M., Netsky, B;	
XX		
DR	WPI; 1997-226206/20.	
XX		
PT	Human and <i>Saccharomyces pombe</i> protein ubiquitin ligase(s) - involved in cdc25 phosphatase and p53 ubiquitination, and regulate cell growth and proliferation	
PT		
PS	Claim 1: Page 74-77; 108PP; English.	
XX		
CC	Human protein ubiquitin ligases publ (AAW13384), Pub2 (AAW13385) and pub3 (AAW13386) are homologues of fission yeast publ (AAW13387) and were identified from cDNA clones (RAm4740-42) obt. e.g. from a keratinocyte cDNA library. Pub polypeptides can be produced in transfected host cells. They can control the steady state level of cdc25 phosphatase, the degree of CDK kinase (e.g. cdc2) dephosphorylation and the steady state level of p53 (controlling the degree of cell cycle regulation of p53). They can regulate cell or tissue differentiation, or cell growth or proliferation by affecting other proteins, can be a specific antagonist of wild-type protein function and may be used as immunogens to elicit a specific immune residue.	
XX		
RESULT 5		
AB31477		
ID	AB31477 standard; Protein; 748 AA.	
XX		
AC	AB31477;	
XX		
DT	20-APR-2001 (first entry)	
DE	Amino acid sequence of a human Smurf2 polypeptide.	
XX		
KW	Smurf1; Smurf2; Smad signal transduction; bone morphogenic protein; BMP; transforming growth factor-beta; human; TGF-beta; chondrogenesis; osteogenesis; blood differentiation; cartilage formation; hair growth; neural tube patterning; retinal development; heart induction;	
KW		





PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-019123.  
 PR 19-MAY-2000; 2000US-020515.  
 PR 07-JUN-2000; 2000US-020467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-AUG-2000; 2000US-0221496.  
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 PR 14-AUG-2000; 2000US-0225266.  
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 PR 18-AUG-2000; 2000US-0226268.  
 PR 22-AUG-2000; 2000US-0226681.  
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 PR 22-AUG-2000; 2000US-0227182.  
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 PR 08-SEP-2000; 2000US-0232080.  
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 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0234240.  
 PR 14-SEP-2000; 2000US-0234241.  
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 PR 14-SEP-2000; 2000US-0234241.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235084.  
 PR 27-SEP-2000; 2000US-0235034.  
 PR 29-SEP-2000; 2000US-0235036.  
 PR 29-SEP-2000; 2000US-0236302.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.

PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241887.  
 PR 20-OCT-2000; 2000US-0241898.  
 PR 20-OCT-2000; 2000US-0241909.  
 PR 20-OCT-2000; 2000US-0241936.  
 PR 01-NOV-2000; 2000US-0244637.  
 PR 01-NOV-2000; 2000US-0244637.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
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 PR 08-NOV-2000; 2000US-0246566.  
 PR 08-NOV-2000; 2000US-0246577.  
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 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
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 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 05-DEC-2000; 2000US-0251160.  
 PR 01-DBCC-2000; 2000US-0251160.  
 PR 01-DBCC-2000; 2000US-0251963.  
 PR 05-DBCC-2000; 2000US-0251963.  
 PR 05-DBCC-2000; 2000US-0251988.  
 PR 05-DBCC-2000; 2000US-02556719.  
 PR 06-DBCC-2000; 2000US-0251479.  
 PR 08-DBCC-2000; 2000US-0251856.  
 PR 08-DBCC-2000; 2000US-0251868.  
 PR 08-DBCC-2000; 2000US-0251869.  
 PR 08-DBCC-2000; 2000US-0251989.  
 PR 08-DBCC-2000; 2000US-0251990.  
 PR 11-DBCC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2000US-0259678.

XX (HOMA-) HUMAN GENOME SCI INC.  
 PA  
 RI Rosen CA, Barash SC, Rubin SM;  
 XX  
 DR WPI; 2001-581633/65.  
 DR N-P5DB; ABKA3631.  
 XX  
 New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -  
 XX  
 PG Claim 9; SEQ ID No 819; 837PP; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein, (II) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, respiratory disorders involving neovascularisation e.g. malignancies, acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 57.6%; Score 2236; DB 22; Length 514;  
Best Local Similarity 80.7%; Pred. No. 8.8e-211; Mismatches 414; Indels 4; Gaps 4; Matches 414; Conservative 43; Mismatches 42; Indels 14; Gaps 4;

Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| 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DE Drosophila melanogaster polypeptide SEQ ID NO 10152.  
XX Drosophila; developmental biology; cell signalling; insecticide;  
CC KW pharmaceutical.  
XX OS Drosohila melanogaster.  
XX PN WO200171042-A2.  
XX PR 27-SEP-2001.  
XX DE 23-MAR-2001; 2001W0-US09231.  
XX PT Venter JC, Adams M, Li PWD, Myers EW;  
XX XX DR WPI; 2001-65680/75.  
XX N-PSDB; ABL0523.

PR New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions - Disclosure; SEQ ID NO 10152; 21PP + Sequence listing; English.  
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interaction in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB01841-ABL175) and the encoded proteins (ABB5737-ABB7072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).  
Sequence 1035 AA;  
Query Match 53.3%; Score 2069; DB 22; Length 1035;  
Best Local Similarity 41.2%; Pred. No. 8.6e-134; Mismatches 435; Indels 304; Matches 104; Conservative 104; Mismatches 145; Indels 372; Gaps 15; Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 8  
ABB6120

ID ABB61120 standard; Protein: 1035 AA.  
XX ABB61120;  
XX XX  
DT 26-MAR-2002 (first entry)

228

-- 227  
26-MAR-2002 -- 227  
XX  
DT 26-MAR-2002 (first entry)

Db	367 STSGNGSGQAQPOASASNGWTQEDAATTSPSITSPRHQSOSPPTPNISPAPVTPSAN	425	PR 19-JUL-2000; 2000US-0620325.
QY	228 -----	227	PR 01-SEP-2000; 2000US-0659336.
Db	427 GNTVSPNANSTPAGSGGSSRSYRATPQSCRSASSRQQGESSTRRSSRTRANGTG	486	PR 15-SEP-2000; 2000US-0663561.
QY	228 -----	227	PR 20-OCT-2000; 2000US-0693325.
Db	487 GGGGGGSGGORYASAAIAANQARPFLDLPQGYEMRTIQGQVYFTHIPGVSTWHDPRI	546	PR 30-NOV-2000; 2000US-0720422.
QY	260 PRDLANS -TCNCDELGPPLPGWERTSVTUSGRILYVDHNRTQFTDRHNM-----	309	XX (HYSE-) HYSEQ INC.
Db	547 PRDFEDETOHLLTDATGPLPSWGWEOKTASGRVVFUDHNRRTQFTDPLSSGSILOMIRRTG	606	PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
QY	310 --NHQCOLKEPSQPLPLPS-----	328	PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
Db	607 VPPTERANACTAPPSATATPSAAAAPPQATPASNATPTLTITNNPPRIVPDLPG	666	PI Xie AJ, Yang Y, Weibrant T, Goodrich R;
QY	329 SLEDBELPAQRYERDINQKVKVRHELSIQPOAHCRIEVSREIFPESYRQIMRK	388	XX DR WPT; 2001-476283/51.
Db	667 LIEGADL-LIKYRDVLGKRALTEQTLQMQPSQHCRLESNEPEESTLIMORAK	725	DR N-PSDB; AAK52010.
QY	389 DIKKRMLVKRKGEEEDYDGCVAREWLYNQHMLNPYGLFOYSTNDIYMQINPDSIN	448	XX Nucleic acids encoding polypeptides with cytokine-like activities,
Db	726 DMRKLMVKYKGEGEDLYDGCVAREWLYNQHMLNPYGLFOYSTNDIYMQINPDSIN	508	XX useful in diagnosis and gene therapy.
QY	449 PDHLSYFHFGVGRINGLAVFHGYINGGFTVPPYKQLGKPIQLSDLESPVDEBHKSLWI	785	PS Claim 20; Page 3847; 6221PP; English.
Db	786 PDHLSYFHFGVGRINGLAVFHGYINGGFTVPPYKQLGKPIQLSDLESPVDEBHKSLWI	819	XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
QY	509 LENDITPVHDTCVHNAAFGRLQHKLKPGRNPNVPTENKEVYRLYNNWRMGEIA	568	CC encoded polypeptides (AAK78323-AM80302) that exhibit activity elating to
Db	820 LESNISGIIISTSFVENVNSHGAJVYHVELKPGGASIPVTEENKEVYRLYNNWRMGEIQ	879	CC cytokine, cell proliferation or cell differentiation or which may induce
QY	569 OFLAQKGFFELIOPHLLPQDELELLIGGDKIDLNWASNTRKHCTADSNIVRMF	628	CC production of other cytokines in other cell populations. The
Db	880 OFLAQKGFFELIOPHLLPQDELELLIGGDKIDLNWASNTRKHCTADSNIVRMF	939	CC polymides and polypeptides are useful in gene therapy, vaccines or
QY	629 WQAVETFDEERRARLIQFVTGSTRPLQGKALQGSTGAGRGLFTHL-IDANTNLPK	687	CC peptide therapy. The polypeptides have various cytokine-like activities,
Db	940 WQVVSYSYSSMRARLQFVTGSSRVPLQGFRALQGSGTAVGRALFTLMDAFTQNLPK	999	CC e.g. stem cell growth factor activity, haemopoiesis regulating
QY	688 AHTCFPRIDIPPYEYEVKJLTAVEETCGFAVE	723	CC activity, tissue growth factor activity, immunomodulatory activity and
Db	1000 AHTCFPRIDIPPYEYEVKJLTAVEETCGFAVE	1035	CC activin/inhibin activity and may be useful in the diagnosis and/or
<b>RESULT 9</b>			
AAW18877			CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
ID AAM78877	standard; Protein; 335 AA.		CC inflammation.
XX			CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
AC AAM78877;			CC (AM8020) are omitted as the relevant pages from the sequence listing
XX			CC were missing at the time of publication.
DT 06-NOV-2-2001 (first entry)			XX
XX	Human protein SEQ ID NO 1539.	Sequence 335 AA:	
DE Human protein SEQ ID NO 1539.			Query Match Best Local Similarity 41.6%; Score 1614.5; DB 22; length 335;
XX			Matches 306; Conservative 4; Mismatches 20; Indels 25; Gaps 2;
XX			QY 168 MEPPAPYDSTGAAAGCNERVESISSQDQLQAPIRNPDVRSLOTLQPNRPHQPE
DT	06-NOV-2-2001 (first entry)		227
XX			Db 1 MEPPAPYDSTGAAAGCNERVESISSQDQLQAPIRNPDVRSLOTLQPNRPHQPE
DE Human protein SEQ ID NO 1539.			60 QY 228 LPGEYEQTIVQGVFLHTQGTVSTWHDRIPRDLANSNCDEAQLPGLPWEVSTGCR
XX			287
DE Human protein SEQ ID NO 1539.			Db 61 LPGEYEQTIVQGVFLHTQGTVSTWHDRIPRDLANSNCDEAQLPGLPWEVSTGCR
XX			120
XX	Human: cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.		Db 181 IKVLRHEHSLOQPOAHCRIEVSREIFPESYRQIMRMKPRDKLKRMLYKPRGEGLDG
DE Human protein SEQ ID NO 1539.			240
XX			Db 288 IYFDHNRRTQFTDPLHMHMHQQLKEPSQPLPLPBGSLDEELPAQRVERDLYK
XX			347
AC AAM78877;			Db 121 IYFDHNRRTQFTDPLHMHMHQQLKEPSQPLPLPBGSLDEELPAQRVERDLYK
XX			180
DT 06-NOV-2-2001 (first entry)			QY 348 IKVLRHEHSLOQPOAHCRIEVSREIFPESYRQIMRMKPRDKLKRMLYKPRGEGLDG
XX			407
DE Human protein SEQ ID NO 1539.			Db 181 IKVLRHEHSLOQPOAHCRIEVSREIFPESYRQIMRMKPRDKLKRMLYKPRGEGLDG
XX			240
XX	Human: cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.		QY 408 GVARWLTLICHMLNYQGQYFQYSTNDIYQINPDSINPDLHSLYFHFVGRINGLAVF
DE Human protein SEQ ID NO 1539.			467
XX			Db 241 GVARWLTLICHMLNYQGQYFQYSTNDIYQINPDSINPDLHSLYFHFVGRINGLAVF
XX			298
OS Homo sapiens.			QY 468 HGHVINGGFTVPPYKQLGKPIQLSDLESPVDEBHKSLWILENDITPVLDHTFC
XX			522
PN WO200157150-A2.			Db 299 -----CVPWTLHORG-----LHSALLQAAAGEBAHPALRGIC
XX			330
PD 09-AUG-2001.			RESU
XX			LT 10
PP 05-FEB-2001; 2001WO-US04098.			AAW13385
XX			ID AAM13385 standard; Protein; 766 AA.
PR 03-FEB-2000; 2000US-0496914.			XX
PR 27-APR-2000; 2000US-0560875.			AC AAW13385;
PR 20-JUN-2000; 2000US-0598075.			XX
PR			DT 10-JUL-1997 (first entry)

XX Human protein ubiquitin ligase pub2.  
 XX DE  
 KW Protein ubiquitin ligase; pub2; cdc25 phosphatase; CDK kinase;  
 KW p53; cell cycle; transgenic animal.  
 XX OS Homo sapiens.  
 XX PN WO9712962-A1.  
 XX PD 10-APR-1997.  
 XX PP 04-OCT-1996; 96WO-US15930.  
 XX PR 04-OCT-1995; 95US-0539205.  
 XX PA (COLD-) COLD SPRING HARBOR LAB.  
 XX PI Beach, D., Caligiuri, M., Nefsky, B.;  
 XX WPI; 1997-226206/20.  
 DR N-PSDB; RAT47041.  
 XX PT Human and Saccharomyces pombe protein ubiquitin ligase(s) - involved  
 PT in cdc25 phosphatase and p53 ubiquitination, and regulate cell  
 PT growth and proliferation  
 XX PS Claim 1; Page 80-84; 108pp; English.  
 CC Human protein ubiquitin ligases pub1 (AAW13384), pub2 (AAW13385) and  
 CC pub3 (AAW13386) are homologues of fission yeast pub1 (AAW1387) and  
 CC were identified from cDNA clones (AAW47041-42) obt'd, e.g. from a  
 CC keratinocyte cDNA library. Pub polypeptides can be produced in  
 CC transfected host cells. They can control the steady state level of  
 CC cdc25 phosphatase, the degree of CDK kinase (e.g. cdc2)  
 CC dephosphorylation and the steady state level of p53 (controlling  
 CC the degree of cell cycle regulation of p53). They can regulate  
 CC cell or tissue differentiation, or cell growth or proliferation by  
 CC affecting other proteins, can be a specific (ant)agonist of wild-  
 CC type protein function and may be used as immunogens to elicit a  
 XX SQ Sequence 766 AA;  
 Query Match Similarity 37.6%; Score 1461; DB 18; length 766;  
 Best Local Similarity 40.8%; Pred. No. 4-58-134;  
 Matches 326; Conservative 118; Mismatches 236; Indels 120; Gaps 20;  
 QY 4 SIKIRLTVLCKNLAKEDDFRLPDPFAKIVVWPDGSGOCHSISTDVTKNTDPKRNQHLYVG 63  
 Db 7 SRRIRTVIADVADGLYKRDVRFPDPFPAVITVDFGE-QTHHTAIKKTLNPYMMETFEVNT 65  
 QY 64 KTDSTIVTSMWHKKHHKKOAGELGFCVRLNSAISRLKDTGYGRLL-DLCKLNPSDPAV 121  
 Db 66 DNSTIAIQVFDOKRP-KKKJGFLGVINLRVGDVLDLAIIGDEMILIDUKKIN-ENTVV 122  
 QY 122 RQQIVVSLQ-----TRDRIGTGGSVUDGRQLNEGTYED 157  
 Db 123 HKIIINLNSTAQLTHQVRSAAASGARTORTSITNDPOSSKSSVSRNPASSRAGSPTRD 182  
 Qy 158 SGPG-----RPSCFMEG ... PAPY ... TSTG-----AAR 182  
 Db 183 NAPASPDASPRPTSSPFERDQYGRLLPGPGRERCTDNLGRYVYDHNTRSTTWRPNLSSVA 242  
 QY 183 GGGNCRFVSESS-----ODQLQAQRIRNPDVGRGSIQTPONPRPHQSQBLPEGYEQ 234  
 Db 243 GAAAEHLHSASSANNTEGVQPSSENAAIRTEASUTSMTAG-----SERLICWEQ 295  
 QY 235 RTTVOQGVYFAHTQGYSTMDPRTDINSVN-----CDELGPLPQPGWEVRT 283  
 Db 297 RYTPEGPRPYFDHNTITTWDPDQQYVTSYSGGPNATIQQPVPSQ1QGPFLSGWERT 356  
 QY 284 VSGRIFTVDHNRTQFTDPRHLHMHOOLQKERSQSPFLPREGSLERDELPQAVERD 343  
 The invention relates to constructing (M1) a strain of diploid fungal

Do 357 NTAVVTFDPAHKTWTMDPR-----LPS---SL-DQNTP--QYKRD 392  
 OY 344 LVQKLUVRLHLSLQOPOACHRCIEVSREBIFEEFSYRQTMKOREMPKDKEKLRKAVKFGBEG 403  
 Db 393 FRRKLIVLPSQPAI-HPLPQOCHIKVTRRHIFEDSYAELMROSATDLKRMKIFGDRGD 451  
 OY 404 LDYGGVAREWVYLCHEMMLNPYGYGFOYSTDNTMLQNDSSINPDHSYHFVGIMG 463  
 Db 452 LDYGGLSEKYPFLSHEMFNPYCYLPEYSVDNVTLQINPHSGINPERHNFFIGRIVG 511  
 OY 464 LAVFHGHTYINGSFPTWPFYKOLKGKTOQSLESTDPKLRSLWLENDITPVDLHPCV 523  
 Db 512 LAIFHRRFVDAFFVSYKNILOKETVLDQMSDADYTRSYLWILDNDITGVLDLIPSV 571  
 OY 524 EINAFGRLIQLEKLPGRNPNYPTENKVKETVRLYUNWPMRGIEAQFLALQKPNELIPQ 583  
 Db 572 EDNGFGEVUVTDLKPGRNTBVTEENKREYVDLVTVW-TQKRIEBOQFAFHFGSELPQ 630  
 OY 584 KULPKFQKELLIQGGLKIDNPKNSVTRLKICAVDSNIVRMFWQAVETDEERARR 643  
 Db 631 ELINNEDPERELLGICSEIDMELKWDKHDYRSYSENQITKWFELWDENEKSSLR 690  
 QY 644 LQWVTSRVEQFQKALQSTGAQPRHTIHLDANTDNPQHTERENRIPPEY 703  
 Db 691 LQTTGTSRIPNGFKDQSD--GPRKTIKA-GBPNKLPAHNTENRLDPPYTK 746  
 OY 704 EKVYEKULTAVETCTGFAVE 723  
 Db 747 KOLDHKSLIAVEETFGQE 765  
 The invention relates to constructing (M1) a strain of diploid fungal

RESULT 11  
 ABP73459 standard; Protein; 832 AA.  
 ID ABP73459  
 AC ABP73459;  
 XX DT 30-JAN-2003 (first entry)  
 XX DE Candida albicans essential protein SEQ ID NO 7296.  
 XX KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;  
 KW signal transduction; DNA replication; cell division; growth;  
 KW proliferation; Candida albicans; fungicide; antifungal.  
 OS Candida albicans.  
 XX PN WO200253728-A2.  
 XX PD 11-JUL-2002.  
 XX PR 26-DEC-2001; 2001WO-US49486.  
 XX PR 29-DEC-2000; 2000US-059128P.  
 PR 22-FEB-2001; 2001US-0792024.  
 PR 22-AUG-2001; 2001US-314050P.  
 XX PA (ELIT-) ELITRA PHARM INC.  
 XX PI Roemer, T., Jiang, B., Boone, C., Bussey, H., Ohlsen, K.;  
 XX DR WPI; 2002-566694-60.  
 DR N-PSDB; ABZ2209.  
 XX PT Constructing strains for identifying gene products as effective targets  
 PT for therapeutic intervention, by inactivating in the strain one allele  
 PT of a gene and placing other allele of the gene under conditional  
 PT expression -  
 XX RS Claim 44; SEQ ID NO 7296; 167pp + Sequence listing; English.  
 XX

cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an anti-fungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biocytinetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans and for treating infection by C. albicans. The present sequence is that of an essential Candida albicans protein used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.

XX Sequence 832 AA;

Query Match 37.0%; Score 1436.5; DB 23; Length 832;  
Best Local Similarity 38.4%; Conservative 124; Mismatches 233; Indels 167; Gaps 21;

Matches 326; Conservatve 124; Pred. No. 1.3e-131; ID ABJ26104 standard; Protein; 869 AA.

Qy 7 IRLTVLCAKNIKKAKPFRFLDPFAKIVWGGSGQCHSTDVTKNLDPKWQNQHLYVKTD 66  
Db 17 INVKVVAEESLYKRDYFQDPAVLTVPQG-QKTTITAKKTINPYWNEN-FOKED 74

Qy 67 SI-TISWVWAKNIKKQGAGFLGCKL-LSSAHLRKLTGQI-L-DICKLNPSDTAVR 122  
Db 75 SILVIOQFDQKTF-KKDQDFPLGVINVRGDDVILSNSSEETIDDKKSN--ENLAVS 131

Qy 123 GOIVVSIQ-----TRD-----RIGTGGVVDCRILE 149

Db 132 GLIIVVISHNNSNGGAGVATRTRGASSNNATITGGVNLIGSATTAATNQAS 191

Qy 150 NRGTV-YEDSPGR--PLCFCMESPAPYDSTGAAAGGCNCREVESQSODRIQAGRLR 205  
Db 192 SDATVGANGSGPTTSIPLPGQHPETATPFGGAAGRAGMASQRQISSFDQQGRLLPPGWER 251

Qy 206 NPDVRG-----SQTPOPRPHQSP----- 226

Db 252 RTDNFGRTYYVDHSRNTTWORPALHQSETBERGOORQSETEAERRHGRTRPGEHSVSP 311

Qy 227 -----ELPGYBQRTIVGQV 242

Db 312 LPTGSQNSITSGNTVNAASGANTTPVNPAALAVSMAASGATTSGLGELPQWEFTTGP 371

Qy 243 YFLATQGQSVWHDPRIPRDLNSVN-----CDELGELPPGNEVSTVNSGRIVUDH 293  
Db 372 YFVDHNRTTWTWDRPRQYVIRTGGNTTQQQPSQLPSEGWSERMNTARVYFHD 431

Qy 294 NRRTQFDPRLHHIMHQCOLKERSQPLPSEGSLDEBPAQYRVDLVLQKLVLRH 353

Db 432 NTTKTTDDPR-----LPS-SL-DQNV-QYRDRFRKVIYRS 467

Qy 354 ELSLQQQOQAHGRIEVSREBEEFESYRQIMVCRPKDQKKEMLVPRGERGQGDYGGVARW 413  
Db 468 QPAL-RILPGQCHIKFRDHIFEDSQEIQINRQTPEDLKGKLMKEDGERGQGDYGGVSREF 526

Qy 414 LYLCHEMNPYQGLFOYSTONIYMOINPDSINPDHYSYFHGRINGLAVPHGHYN 473  
Db 527 FFLISHDMVNPNFCYLFFBISHNYLQINPENGSGHINPEHLYTFKIGRVVGLGVFRRFLD 586

Qy 474 GGTVPFKQKGKPIOLSPSVDPLHSLIWLENDITPVUHTEVWHAAGRILQ 533

Db 587 APFGVGALLYKMMHLKKVVLQDMEGVDAEFYRSIKWILDNTGIDLTPSAEESRGTE 646  
Qy 534 HELKPNGNRNPVTEBNCKEYRYLYVWWRFMGEGIEAQFLAQKGFMELQPHLKFQDCE 593  
Db 647 VDLKPGGEDIETBENKHEVYLTERWRSRVEQFKATIDGFLNLIQELVNFDE 705  
Qy 594 LEITIGGSDKIDNWKSENTRKHCYADSNIVRWPWQAVTFDERRAMLUQFTGSTRV 653  
Db 707 LEILIGGIAEIDCWDWKHTDYRQENDQVQWMFKCINCNEWDSBQKALUQFTGTSI 766  
Qy 654 PLOCFKALQGSTGAAGRFLPHTLIDANTDLPKARTCERIDPYYEYKLEKLU 713  
Db 767 PVNGFKDQGSD---GPRRFTEKA-GEANQLPKSHTCFENRVDLPPYTYDYESLKQUTA 822  
Qy 714 VEETVGFPAVE 723  
Db 823 VEETVGFQEQB 832

RESULT 12  
ID ABJ26104  
XX ABJ26104 standard; Protein; 869 AA.  
AC ABJ26104;  
XX DT 16-APR-2003 (first entry)  
XX DE Aspergillus fumigatus essential gene protein #762.  
KW Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response.  
XX OS Aspergillus fumigatus.  
XX PN WO2028090-A2.  
XX PD 31-OCT-2002.  
XX FP 23-APR-2002; 2002WO-US13142.  
XX BR 23-APR-2001; 2001US-205697P.  
PR 27-ARR-2001; 2001US-207066P.  
PR 05-JUN-2001; 2001US-205890P.  
PR 09-TUL-2001; 2001US-03899P.  
PR 31-AUG-2001; 2001US-31652P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Jiang, B., Tishkoff, D., Zamudio, C., Broshkin AM, Hu, W., Lemieux SM;  
XX WPI: 2003-093124/08.  
XX New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer - Disclosure; Page -; 175pp; English.  
XX The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterization, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and

CC making oligomers for attachment to a nucleic acid array for examination  
 CC of expression patterns for raising anti-protein antibodies, as an  
 CC antigen to raise anti-DNA antibodies or to elicit another immune  
 CC response, and for identifying polynucleotides encoding the other protein  
 CC with which binding occurs or to identify inhibitors of the binding  
 CC interaction. The polypeptides may be used to raise antibodies or to  
 CC elicit immune response, as a reagent in assays designed to quantitatively  
 CC determine levels of the protein in biological fluids, as a marker for  
 host tissue in which pathogenic organism invade or reside, and to  
 CC isolate correlative receptors or ligands in the case of virulence  
 CC factors. This sequence represents a protein of one of the essential genes  
 CC of Aspergillus fumigatus of the invention.

XX SQ

Sequence 869 AA;

Query Match	34.6%	Score 1345; DB 24; Length 869;
Best Local Similarity	35.9%;	Pred. No. 1.Se-122;
Matches	317;	Conservative 123; Mismatches 236; Indels 208; Gaps 26;
QY	11	VLCAKQLAKDFR-----LPDPFRKIVWDGSGQCHSTDVKNT 49
Db	23	VIAADGLYKDVERKSYVAILLYVRLITGAGFEDPPEAVATVGE-B-QHTTSVIKT 81
QY	50	DQPKHQHLYVKGUDSITISVANHKKHKKGAGFGCVRL-----
Db	82	LNPYNTNEMPRWNRVNEQDSILAQIFDQKTR-KKDQGELGVINVRIQGMGDEGSI 140
QY	94	---SNAISLILK----DTGYORUDCKLNPSDTDAVQGIVVSQI----- 93
Db	141	PIRKSDVSKLTFRLILTEFLTRDKSN--DNLVHGKLINISTNSITPNHQANG 198
QY	132	--DRDRTGGSVWDCRGJLN-----EGTVYED--SGPG-----RPLSC 166
Db	199	IHRSHYQSSIS---SGLIVEQVARSSHPAASGAPVDPASNPSLNPFQRYPSTRPSST 254
QY	167	FMEEP-----PTVTDGAAAG-----GNCREVE-----SP 193
Db	255	AAAPASHAGAAVSNHSRSRTNLSFSDESGCRGPAGWERREDNLGRTYVDHNRRTTWTRP 314
QY	194	SQDQLQQAQILRN-----PDVR--GSLQTQNPYPHQGP----- 226
Db	315	SSNYNHHAQSOSEANMOLERRAHOSRMVLEDTGANSNPNLPESSOQAHTPAGGSANAV 374
QY	227	-----ELPEGYMTQRTVQGQVYFLHQTGTGSTWDPR-----IPRDLSV 266
Db	375	SMMATGATTAGTGEGLPPGHEQRTPEGRV----- 434
QY	267	N-----CBIGLPLPGWHRVSRSTVSGRTYFVDHNRRTQFTDPRHLHMHQCOLKEPS 319
Db	435	NTTQQQPVSVOLGPFLPSGWMLNTARYFVDHNRTKTWDPR----- 479
QY	320	OPLPLUSESEGGLDEDLPAQYERDILQVKVLUHBLSQPOQHGRHCRIEVREEEFEESY 379
Db	480	----LPS--SL--DQGP--QYKDFRKLHYFRSQPAL-RIMSGQCHVKAARNNIFEDSY 529
QY	380	RQIMKRPKQKLUMLKMKFEGEGLDYGCAWARENLYLCHEMNPYQGLPQYSTNDIYML 439
Db	530	ABMRQASPOLKKLMKFDGEGDGLDYGGLSGERFFFLSHEMNPYCFLEYSAHDNYTL 589
QY	440	QINPQSSINDPHLSRTHFVQRINGLAVFHQHYINGFWPYQQLSKPQLDSLSDVP 499
Db	590	QINPQSGVNPHEHLYTFKTFGRVGLAIFRFLDSFFGAFAYKOMLRKVKVSLQDMBGDE 649
QY	500	ELHKSTWVILEENDITPVLDTFCVHNATGRLOHELNGRNPVTEBNKKEVYLVN 559
Db	650	DHHRNLTWMDINDSIVLTLTSEVDEKEGERRTDLKPGROUPVNVENKAEVLYUTE 709
QY	560	WRFMRGTEAOFLALQGNELTIPOLIKKOPDKKELELITGLQXIDNDWKNTRLKHCV 619
QY	710	WKIVKRVVEQNAFMGSGNLIPADLVNVEDERLLELJGADIDVNDWKGHTDGYQ 769
QY	620	ADSNIVFWQFOVETDEBERRARLILQPVGSTRPLQGKALQOSTGAGAERPHTHID 679

Db 770 ESDEVIONFWKITVRSMDAEKSRUQIQTGTSRIPVNGEFDLOGSD--GPRRFTEK-S 825  
 QY 680 ANTDNUPKAKTCPNRDIPIYESEKLYKLTVEEGFGATE 723  
 ; |||:|||:|||:|||:|||:|||:|||:|||:  
 Db 826 GPPAALPKSHGPNRUDLPPYKSYTLEHNSLVEETGFGS 869  
 RESULT 13  
 ID AAV30949  
 ID AAV30949 standard; Protein; 854 AA.  
 XX AAV30949;  
 AC AAV30949;  
 XX DT 21-OCT-1999 (first entry)  
 XX Murine E3 ubiquitin protein ligase protein.  
 XX E3 ubiquitin protein ligase; h-E3 UPL; antiinflammatory; antidiabetic;  
 KW immunosuppressive; neuroprotective; cytostatic; anticancer; cardiotonic;  
 KW immunomodulator; antiviral; treatment; screening; gene therapy; cancer;  
 KW inflammation; autoimmune disease; neurological disease; apoptosis;  
 KW peripheral vascular disease; hematopoietic disorder; angiogenesis; cachexia;  
 KW pulmonary disorder; diabetes; viral infection; murine.  
 XX OS Mus sp.  
 PN WO9940201-A1.  
 XX PD 12-AUG-1999.  
 XX PP 02-FEB-1999; 99W0-GB00353.  
 XX PR 30-APR-1998; 98US-0070060.  
 PR 05-FEB-1998; 98US-0073839.  
 XX PA (ZENE ) ZENeca LTD.  
 XX PI Ghildayal N, Hustad CM;  
 XX DR WPI; 1999-508506/42.

PT New human proteolytic accessory enzyme and its modulators useful

PT for treating disease conditions like inflammation or autoimmune

PT diseases

XX Disclosure; Fig 4; 95pp; English.

XX This invention describes a novel human polynucleotide (I) which encodes a

CC ubiquitin protein ligase, h-E3 UPL (II). The products of the invention

CC have antiinflammatory, immunosuppressive, neuroprotective, cytostatic,

CC antiarhythmic, immunomodulator, antidiabetic, antiviral and cardiotonic

CC activity. The products of the invention can also be used for treating

CC patients with disorders mediated by the biological and/or pharmacological

CC activity of h-E3 UPL. The nucleic acid sequences encoding E3 UPL are used

CC in expression systems as assay for agonists and antagonists for the E3

CC UPL protein. The h-E3 UPL protein is used in screening assays to identify

CC blockers and antagonists. They are also used in gene therapy. Specific

CC modulation of biological and/or pharmacological activity of novel h-E3

CC UPL via administration of a modulator or heterologous expression, is used

CC for treating physiological conditions like inflammation, autoimmune

CC diseases, neurological disease, apoptosis, endothelial cell physiology

CC (e.g., proliferation, differentiation), peripheral vascular disease,

CC angiogenesis, cancer, hematopoietic disorders, arthritis, cachexia,

CC leukemia, pulmonary disorders, diabetes and viral infection. The

CC nucleotide sequences which encode h-E3 UPL may also be employed in

CC analysis to map chromosomal location, e.g., screening for functional

CC association with disease markers. They are also used as screening tools

CC in the identification of appropriate human subjects and patients for

CC therapeutic clinical trials. The sequences can also be used to detect the

CC presence of the mRNA transcripts in a patient or to monitor the

CC modulation of transcripts during treatment. This sequence represents the

CC mouse E3 ubiquitin protein ligase protein described in the method of the

CC	invention.	
XX	AC	AY30948;
SQ	Sequence	854 AA;
Best Local Similarity	33.9%;	Score 1318; DB 20; Length 854;
Matches 316;	Conservative 35.4%; P-Fred: No. 6	8e-120; Mismatches 229; Indels 220; Gaps 29;
Db	6 KIRLYVCAK-NLAKKDFRFLDPFAKIVWQSGQCHSTDVKNLDPKNNQHDLVYK 64	9 QLQTIVSALKLKENKVNKFV-SPVYETD-GOSKTECNCNTNSPKKQPLTVIP 65
QY	65 TDSTISVWAKKKHKKGAGFGCCVRL--L-SNAISRLKOTGYQR---- 107	66 TSKICFRRVSHQTL--KSDVLLTAGDIVYTLKSNNMKBEVNTLQLWGDKRPTM 122
Db	108 -LDLICKLNPSDTDAVGIVVVS-----LQTRD-RIGGGS--VVDCR 145	123 GDL SVC--LDGQVBEAVVNGETCSSESTQNDGCRARRDRVSTNGEDPEVAAS 178
QY	146 G-----LLENESVYVESSGRPLSCFMEEBAPYI-----DSTG 179	147 GENKKRANGNNPSLSNGG--FKSRPPR----SRPPPPPRPASVNGGSPSTNSDQ 231
Db	179 LRNPVYRGEL-----QTPQNRPHGQSPBILPECYBQRTVQGVYFLHTQGSTMH 255	180 AA-----AGGGNCRFVNSPSQ-----DORLAQAR 203
QY	288 ---DQHGRVYVYDHVEKRTTWRPPE---PLPGWERRVUNMGRIYVYDHFTRTTWQ 338	256 DPRIP-----RDL----NSVNODELGPPLPOWER 281
Db	339 RPTESVRVNEQWQLQRSQLOGAMQFNQRETYGNQNLFAQNKEPDPGLPPLPGWEKR 398	399 TDNSGRVYVFHNTRITQMEPR----SQGQLINE--KPPJEGWMRFTWDGIFYFVDH 450
QY	507 TLFEDSFQOMSFSPQDLRRLWVIFPGBEGEGLDGYGVARENWFLLSHEVLMVPMCYLFEA 566	325 -----PSEGSLDEERLPAQYERDILQKUQVLR--HEILSLOCOPQACHRCBTEVSRE 372
Db	451 NRRATYIDPRTGSAALDNGQTAIVRDFKAKYQFRFWCCQAMQ--HIKITVTRK 506	433 TDNTWMLQINPDSINPDHSYHVFGRIMGLAVFHRYINGPPTPYKQOLGPIQS 492
QY	373 EIEFSYRQNMKMPKDQKLKRMVKFRBEGEGLDGYGVARENWFLLSHEVLMVPMCYLFQS 432	567 GDKNYCQLOINPASYINPDHRYKFRFIGKTMALPHGKFDITGFSLPPFYKRINKPVLK 626
Db	507 TLFEDSFQOMSFSPQDLRRLWVIFPGBEGEGLDGYGVARENWFLLSHEVLMVPMCYLFEA 566	493 DLESIDPELHKSLWILENDITPV-LDHTPCVBNAGRILQHLEKNGRNPVTEENKK 551
QY	627 DLESIDPEFVNSLWAKKNNIEBCEGLEMFYSVKEIIGBKEKGHDLPNGGNVILVENEKE 686	627 DLESIDPEFVNSLWAKKNNIEBCEGLEMFYSVKEIIGBKEKGHDLPNGGNVILVENEKE 686
Db	552 EVRLVNVWTFMRGTEAQIQLAQKGKFNEITPQHLIKPDRQKSEBLIGGLDQKIDAWKS 611	687 EYIRMAEWNLRSRGYEEQDQAFGGFNEILPQQLQYDAKELEVUICGMQBDLNDWQR 746
QY	687 EYIRMAEWNLRSRGYEEQDQAFGGFNEILPQQLQYDAKELEVUICGMQBDLNDWQR 746	612 NTRLGCVADASNTVERFWQVETDFBERRAIIQVFTGTRPLQGRKALQOSTGAGPR 671
Db	747 HAIYHYHTRFSKQIMWFQTKEDNEKURLUQFVIGTCRAPPVGGADMSN--GPO 803	672 LIFTIHIDANNDLRAKHTCFNRIDIPPYSEYKLYEKULATAVEETGOFAYE 723
QY	804 KFCIBRY-GENWLPRSHICUFNRLDPPKSYIQUKRLIAEETEFGQS 854	804 KFCIBRY-GENWLPRSHICUFNRLDPPKSYIQUKRLIAEETEFGQS 854
Db		
RESULT 14		
AY30948		
ID AAY30948 standard; Protein: 852 AA.		
XX		

This invention describes a novel human polynucleotide (I) which encodes a E3 ubiquitin protein ligase, h-E3 UPL (II). The products of the invention have antiinflammatory, immunosuppressive, neuroprotective, cytoprotective, antiarthritic, immunomodulator, antidiabetic, antiviral and cardiotonic activity. The products of the invention can also be used for treating patients with disorders related to the biological and/or pharmacological activity of h-E3 UPL. The nucleic acid sequences encoding h-E3 UPL are used in expression systems as assay for agonists and antagonists for the E3 UPL protein. The h-E3 UPL protein is used in screening assays to identify blockers and antagonists. They are also used in gene therapy. Specific modulation of biological and/or pharmacological activity of novel h-E3 UPL via administration of a modulator or heterologous expression, is used for treating physiological conditions like inflammation, autoimmune diseases, neurological disease, apoptosis, endothelial cell physiology (e.g., proliferation, differentiation), peripheral vascular disease, angiogenesis, cancer, hematopoietic disorders, arthritis, cachexia, leukemia, pulmonary disorders, diabetes and viral infection. The nucleic acid sequences which encode h-E3 UPL may also be employed in analysis to map chromosomal location e.g., screening for functional association with disease markers. They are also used as screening tools in the identification of appropriate human subjects and patients for



Page 1

osteoarthritis, gouty arthritis and other arthritic conditions, sepsis, respiratory distress syndrome, cerebral malaria, chronic pulmonary inflammatory disease, silicosis, pulmonary sarcoidosis, bone resorption diseases, reperfusion injury, graft versus host reaction, allograft rejections, Crohn's disease, ulcerative colitis or pyrexia in addition to a number of autoimmune diseases such as multiple sclerosis, autoimmune diabetes, systemic lupus erythematosus and ENL in leprosy, HIV, and AIDS. This sequence represents a human KIAA1 ligase which is used in the

Db	853	FVIGISRKPMPNGPAEYGSN--GPQSFLIVEQW-GTFBKUPRAHTCNRDJPPIFEEF	908
QY	706	LYKVLUTAVEREGCF	720
Db	909	LWDKLQMAIENPQGF	923

Query	Match	Score	Length	927;
	Best Local Similarity	33.6%	Pred:	No. 5.1e-14;
	Matches	307;	Conservative	129;
	N mismatches	239;	Indels	240;
	Gaps	28;		
QY	7 IRLITVCAKOUAKDFRFLDPFVKIV---VGSQGCHSTPVTQKTDPKN-----	55		
Db	84 VRVRVIAIGLAKKODLGASDPYVTPYDPMNGVLTQVTKHKKNSNPKEETFLFRV	107		
QY	56 ---QH-----YDLVKTID-SITSVW-----	83	HKKHKKG	167
Db	108 HQQHQHILFEVDENRLTRDPLGQDVPLYPLPUTEPRLERPYTFKDFVHLPRSHKSRV	216		
QY	114 -----NPSI---TDAVRGQTIVSIIQ---TDR 134			
Db	217 PSPLPFGWERQDIIGRTTYVNHSSRQRQWKRTPQDNLTDENGTLQLQQRATTRRQ	276		
QY	135 IGTGGSVUDRGERLLEN-----EGTVVTDG-PGRPLSCFMEPARPYD-----	176		
Db	277 ISBETSEVDNOESEBNWEIRED3BATMISQAFPSPPPSNLDPVTLAELNARLTIFG 336			
QY	177 -----STGAAGGGNCR-----PVEPBS-----	204	QDPLQQLR-----	204
Db	337 NSAVSPASSNNHSSRGSLQAYTEEQTLPVLLPISGLPGLPGWEEKRQDERGRSYVHD	396		
QY	205 -----RNPDVPGQLQTPO-----NRPHQHOSPELBYEQ 234			
Db	397 NSRTTWTKPVIQATWTETSOULSSQSAGQOSRSTSBDQQVTTQPSBIEOCFLPKGEV	456		
QY	235 RTIVQGQVIEHTQGVSTVHDPR--IPRDLSV---NCDELGFLPGWERTSVGRI 288			
Db	457 RHAPNRPFFEDHNNTKTTWEDPRLKPKTIPAHRLKTSQTSNDLGFLPGWERTHINDGRI	516		
QY	289 YFVDHNRITPFDRLHHMNHOOLQKPSQPLPSSEGSLDEELPAQRRERDVLQKL 348			
Db	517 FVYNHNIKRTQWEDPPLNU-----AATGPAPV-----YSRYRKY 553			
QY	349 KYVLRHELSLOOPAOGHCRTEVSREBFEESYRQIMKRPKD-LKCRMVKGPRGEGSDLYG 407			
Db	554 EFRRKUKKQKNDIPNKFEMURRATVLEDSYRIRMVGRADELKARIWIBFGEKLDIG 613			
QY	408 GWAREMLYLQCHEMLMPYQGLFOSTDNTYMOINPNSSI-IPDHSYFHVGRINGLAV 466			
Db	614 GWAREPFLKSEMENPYQGLFEYSAIDWYTLQINPNGLCNEHDHSYFKFGRVAGMAV 673			
QY	467 FHGYHNGGPTFPYKQKPLQSLDSSVPLHSLVWLFENDTPVUDHTCEVN 526			
Db	674 YHGKLIDGFFIRPFYOMLHRKPITADMSVDSVYNSLWILENDPE-IDLRFIDEE 732			
QY	527 AFGRIQHKLPGNGRNPVTEENKEKVYLVNVWRGIGIEOFLAQKGENELIPOHLL 586			
Db	733 LPGQTHOELKGNGSSHIVVNKNKEVYIVIVQFVRVIRQKOMAAKREGFELPQDLI 792			
QY	587 KPPDQKELLIIGGLDKIDLNWKONTRLKH-CVADSNVRFWQAVETDEBERRALQ 645			
Db	793 KTFDENELLELMCGLDGDVNDWREHTKYKNGSYANHGYIQWKFVKAJLMMSEKRRILQ 852			
QY	646 FVTGSTRVPLQCPKAIQGSTGAAGERFLFTIHLIDANTDNLPKAHTCNRIDPPIYESEK 705			

GenCore version 5.1.6  
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**OM protein - protein search, using sw model**

Run on: February 20, 2004, 15:26:11 ; Search time 15:23:66 Seconds  
(without alignments) ; 2007.718 Million cell updates/sec

**Title:** US-10-009-945-2  
**Perfect score:** 3884  
**Sequence:** 1 GSSSIRKILTVLCAKLNKK... . . . . EKLYEKILTAVEETCGFAVE 723

**Scoring table:** BLOSUM62  
**Gapop:** Gapop 10.0 , Gapext 0.5

**Searched:** 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Database :**

Issued Patents AA:\*

1: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:\*

2: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:\*

3: /cgn2\_6/prodata/1/aa/6A\_COMB.pep:\*

4: /cgn2\_6/prodata/1/aa/6B\_COMB.pep:\*

5: /cgn2\_6/prodata/1/aa/PCITUS\_COMB.pep:\*

6: /cgn2\_6/prodata/1/aa/backtles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match	Length	DB ID	Description
1	2913.5	75.0	735	3	US-08-539-205A-2
2	2913.5	75.0	735	4	US-08-539-205A-2
3	1471.1	37.9	766	3	US-08-539-205A-4
4	1471.1	37.9	766	4	US-08-539-205A-4
5	1318.9	33.9	854	2	US-08-391-163A-4
6	1318.9	33.9	854	3	US-08-391-163A-4
7	1301.1	33.5	852	2	US-08-070-060-3
8	1301.1	33.5	852	3	US-08-357-746-3
9	1259.9	32.4	927	3	US-08-895-601-6
10	1228.5	31.6	834	3	US-08-539-205A-6
11	1228.5	31.6	834	4	US-08-392-163A-5
12	1225.5	31.5	906	3	US-08-630-916A-48
13	1047.7	27.0	683	3	US-08-630-916A-46
14	530.5	13.7	874	2	US-08-247-904B-8
15	530.5	13.7	874	3	US-08-767-942A-21
16	509.9	13.1	866	1	US-08-100-692-1
17	509.9	13.1	866	2	US-08-674-030-1
18	473.2	12.2	1083	3	US-08-895-601-5
19	241.1	6.2	3	US-08-345-518C-2	
20	238.5	6.1	472	3	US-08-348-518C-5
21	238.5	6.1	472	3	US-08-476-509B-5
22	162.5	4.2	448	3	US-08-476-509B-2
23	162.5	4.2	448	3	US-08-476-509B-2
24	161.5	4.2	454	3	US-08-348-518C-4
25	161.5	4.2	454	3	US-08-476-509B-4
26	154.5	4.0	55	3	US-08-630-916A-75
27	148.5	3.8	3	US-08-630-916A-84	

**ALIGNMENTS**

RESULT 1  
US-08-339-205A-2  
Sequence 2, Application US/08539205A  
; Patent No. 6005619  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Caligiuri, Maureen  
; ATTORNEY/ AGENT INFORMATION:  
; NAME: Neffky, Bradley  
; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/539-205A  
; FILING DATE: 04-19-1995  
; ATTORNEY/ AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSV-005.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1000  
; TELEFAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 735 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ; US-08-539-205A-2

Query Match 75.0%; Score 2913.5; Length 735;  
Best Local Similarity 72.9%; Pred. No. 1.4e-280;  
Matches 552; Conservative 63; Mismatches 71; Indels 71; Gaps 9;  
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Sequence 839,

Db 59 SDSVTISVNHKKHQAGFGLGCVRLISNAIRLKDGYQRLICKLGPNDNTVRQ 118

Db 125 IVSLOQTDRIGTGGSVWDCRGLIENE-----GTYY----- 155

Db 119 IVSLOSDRRIGSGQVYDSCSFNLDPDEERRTASRGIQVINHTRTQPRPTRP 178

Db 156 --EDSGPGRPLSCPMEEAPAYTDSTGAAGGNCRFVESPSQDQRQAGRLNPDVSSL 213

Db 179 ASEYSSPGRPLSCFDENTPPISSINGATCG-----QSSPRLAERRRSQRHRYM 229

Db 214 QTPONRPGHQSCLPEPYERQTIVQVOVYFLHTQFLGTVSTWHDPRIPRDLNSVNCDELGP 273

Db 230 ---SRTHLHTPPDLPGEYERQTIVQVOVYFLHTQFLGTVSTWHDPVPRDLNSVNCDELGP 285

Db 274 LPGWEWRTSYVSRIFVYDHNRTTOFTDPR---LHHIMNHCOKERSQPLPSESS 329

Db 286 LPGWEWRTSYVSRIFVYDHNRTTOFTDPRUSANLHLVLRQNQKQQQVW----S 341

Db 330 L--EDEELPAQRVERDILVOKULVRHLHSLOOPOGHCRREVSEEFEESEYRIMKR 386

Db 342 LCPDDTCFLTVPRYRDLVOKULKTRBLQOQPOGHCRREVSEEFEESEYRQVMKR 401

Db 387 PKDLKRMKMKFRGEGLDGGVAREWLYLSCHEMLNPYKLFQSTDNIMYLQINPDS 446

Db 402 PKDLKRMKMKFRGEGLDGGVAREWLYLSCHEMLNPYKLFQSTDNIMYLQINPDS 461

Db 447 INPDHLSYFFVGRINGLAWFHGHYINGGTFVPKOLGKPIQSDLESVDPEHLKSLV 506

Db 462 VNPHELSYFFVGRIMGAWFHGHYIDGFTVPUFKOLGKPIQSDLESVDPEHLKSLV 521

Db 567 EAOFIAKQGFNLIPOHKIPDKELLGIDKIDNDWSNTRKHCADSNU 626

Db 582 EAOFIAKQGFNFVIPOLHKTDFEKEBLIGLGKIDNDWSNTRKHCADSNU 641

Db 627 WFWQAVETDEERARLILQFTGSSRVLQPGKALQ---GAAGPRLFTHQIDACTNLP 686

Db 687 KAHTCFNRIDIPPYESYEKUYEKULTAETTCGFAVE 723

Db 699 KAHTCFNRIDIPPYESYEKUYEKULTAETTCGFAVE 735

RESULT 2  
US-09-392-163A-2

; Sequence 2, Application US/09392163A

; Patent No. 6503742

; GENERAL INFORMATION:

; APPLICANT: Beach, David H.

; APPLICANT: Caliguri, Maureen

; APPLICANT: Natsky, Bradley

; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HONG &amp; ELLIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatenIn Release #1.0, Version #1.30

; APPLICATION NUMBER: US/09/392,163A

; FILING DATE: 09/09/2004

APPLICATION NUMBER: US 09/539,205

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: CSV-005.01

REFERENCE/DOCKET NUMBER: 36-709

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 832-1000

TELEFAX: (617) 832-0000

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 735 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-392-163A-2

Query Match 75.0%; Score 2913.5; DB 4; Length 735;  
Best Local Similarity 72.9%; Preo. No. 1-4e-280; Indels 71; Gaps 9;  
Matches 552; Conservative 63; Mismatches 71;

Do 12 VKLRL-----GLPDPFKAVVGDGSOCHSTDIVTQVTPKRNASHDYGK 58

Db 5 TSDITISWMMKKHKHQAGFGLGCVRLISNAISRLKOTGYQRLICKLUNPDTDAVQ 124

Db 59 SDSVTISVNHKKHQAGFGLGCVRLISNAIRLKDGYQRLICKLGPNDNTVRQ 118

Db 125 IVSLOQTDRIGTGGSVWDCRGLIENE-----GTYY----- 155

Db 119 IVSLOSDRRIGSGQVYDSCSFNLDPDEERRTASRGIQVINHTRTQPRPTRP 178

Db 447 INPDHLSYFFVGRINGLAWFHGHYINGGTFVPKOLGKPIQSDLESVDPEHLKSLV 506

Db 582 EAOFIAKQGFNLIPOHKIPDKELLGIDKIDNDWSNTRKHCADSNU 626

Db 603 EAOFIAKQGFNFVIPOLHKTDFEKEBLIGLGKIDNDWSNTRKHCADSNU 641

Db 647 INPDHLSYFFVGRIMGAWFHGHYIDGFTVPUFKOLGKPIQSDLESVDPEHLKSLV 521

Db 651 EAOFIAKQGFNFVIPOLHKTDFEKEBLIGLGKIDNDWSNTRKHCADSNU 626

Db 665 EAOFIAKQGFNFVIPOLHKTDFEKEBLIGLGKIDNDWSNTRKHCADSNU 641

Db 686 WFWQAVETDEERARLILQFTGSSRVLQPGKALQ---GAAGPRLFTHQIDACTNLP 686

Db 687 KAHTCFNRIDIPPYESYEKUYEKULTAETTCGFAVE 723

Db 699 KAHTCFNRIDIPPYESYEKUYEKULTAETTCGFAVE 735

RESULT 3  
US-08-539-205A-4  
; Sequence 4, Application US/08539205A  
; Patent No. 6005619  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Caligiuri, Maureen  
; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSE: FOLEY, HONG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/539, 205A  
; FILING DATE: 04-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSV-005.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1000  
; TELEX/FAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 766 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
; US-08-539-205A-4

Query Match 37.9%; Score 1471; DB 3; Length 766;  
Best Local Similarity 40.9%; Pred. No. 5 4e-137;  
Matches 327; Conservative 118; Mismatches 235; Indels 120; Gaps 20;

Qy 4 SIKRILVLUCKAQLAKKODFFRIPDPPEKIVNGSGOCHSTDVKWNLDPKDNQHDLVYD 63  
Db 7 SRRIRVTVAADGlyKRyVPRDPFAVLTGDE-QTHTTTAIKCILNPWNETEVNT 65  
Qy 122 RQIQIVSIO-----TRDRIIGGSVVDQRLGILENECTVYED 157  
Db 123 HKITIINLSTTAGTQVPSAASGARTORTSITNDPQSSSSVTSRNPAASRAGSPTRD 182  
Qy 158 SGPG-----RPLSCMEE---PAPY----TDSTG-----AAA 182  
Db 183 NAPAPASPERPRFSSSDQGRIPGPOWERDTNQRTYVTDHWRSTTWIRPLSYA 242  
Qy 183 GGGNCRKFVESP-----QDQLQQRNLRNDVGSLQTPONRPHGHOSPELPEGYEQ 234  
Db 243 GAAAEELHSASSASSANVTVGQVBESSNARTEAVLSLTSNATAG----SGELPPGWQ 296  
Qy 235 RTTVQGQVYFLHTOTGVJWHDERRIPDINSTN-----CDEB1GPPGHEVST 283  
Db 297 RYTFEGRPYFVDFHNTTRITIWVDPRLRHIMMHQCLQKERSQPLPPISEASLEDPLPAGRYERD 356  
Qy 284 VSGRFYFVDDNNRTRQFDPRLRLHIMMHQCLQKERSQPLPPISEASLEDPLPAGRYERD 343  
Db 357 NTARYVFDNKTITWDPP-----1PS--SL-DQNV--QYKD 392

RESULT 4  
US-09-392-163A-4  
; Sequence 4, Application US/09392163A  
; Patent No. 603742  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Caligiuri, Maureen  
; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSE: FOLEY, HONG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/392, 163A  
; FILING DATE:  
; PRIORITY APPLICATION DATA:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSV-005.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1000  
; TELEX/FAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 766 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
; US-09-392-163A-4

Query Match 37.9%; Score 1471; DB 4; Length 766;

Best Local Similarity 40.9%; Pred. No. 5.4e-137; Matches 327; Conservative 119; Mismatches 235; Indels 120; Gaps 20;

QY 4 SIKIRIVLWCKAKNLAKKDFFPLPFAKIVDGSGQCHSTDVTNNTDPKRNQHYDLYVG 63  
 Db 7 SRRIRVIVAVADGLYKRDVFRRFPDPFAVLTUDGE-QTHHTAIKTLMPWHEPTENVT 65  
 QY 64 KUDSITISVWHKKHKKRKGQGFLGCRVULNSNAISRLKQTKGYORL--DICKKAPSPDTAV 121  
 Db 66 DNSTIAIQVFDOKKF-KRKGGFLGVINLRVGVDVLDLAIGDEMLTRDKKSN-ENTV 122

Qy 122 RQOIVWSLQ-----TRDRIGGSVYDCGELNEGTYVED 157  
 Db 123 HKLILINLNUSTAQTIQLQPSSAASGARTORTSITINDPOSSKSSVSRSRAGSPTRD 182

Qy 158 SGPG-----RPLSCFMEB---PAPY---TGST-----AAA 182  
 Db : NABAASPSEPRTEFSSEDQYGRPLPGWERTDNLGRTYYVDHNTSTRTWTRPNLSVA 242

Qy 183 GGGNCRCFVES-----QDQLQQLRLENPDYRGSLQTPQRPHGHQSPELPEGEQ 234  
 Qy 243 GAAEALHSSASSANVTEGVQPSNSAARRNEASLTTSNATAG-----SGLPPWEQ 296

Qy 235 RTRVQGQYVFLHNGTQGSIWADPRIPLNSVN-----CDEJQPLPGWEVST 283  
 Db 297 RYVPPGRPVYFHDNTRITWDPRQOYIYSSYQGGSNATTQQQPSVQLGPLGPGWEMLT 356

Qy 284 VSRTIYFDHNRHTTQDTPRHLHMHOCQKERSQPLPSQSLPDSRBLPAQRVERD 343  
 Db 357 NTARVYFDHNTKTTWDDP-----JPS-SI.DQNV-P-QKED 392

Qy 344 LVKLKVURHELSILOPOAGRCIERSRETFEESYQRQNMKRPDKLKRMLWTFRSEBEG 403  
 Db 393 FRRKLIVFLSQFL-HPLPGQCHIKVRNNHFEDSVAEINRQSATDLKERLMKFDGEG 451

Qy 404 LDGGGVAREMWMICHMLNPYGLQYSTNTYQINPDSSENPDHLSYFVGRMG 463  
 Db 452 LDYGGLSREYFPLSHEMFNPFYCUCYBSSYDNTYQINPHSGINPEHNFYKPIGRVIG 511

Qy 464 LAVFGHGYINGGFTVPKQOLQKQPLQDISEVSPLEHKSLVILENDITPUDHFCV 523  
 Db 512 LAFHRREVDAFVUSTYKMIKQKTYQTLQDNESMAYRYSRSLWVLDNDITQDLSV 571

Qy 524 EHNAGFRILQHELKPKNGRNANPVEENKEYVRLYAWRFMRGIEAQFLAQGENELIPQ 583  
 Db 572 EDNGFGEVTITDILKPGNRNGETEENKREYDVWT-TOKRIBEQNFAHEFEGSELIPQ 630

Qy 584 HLLKPKDQEELLTIGGDKDPLNDKNSNTLKHWCWADSNIVRNMQAETFBERRAL 643  
 Db 631 ELJNVDERBLLELIGGISELMDWKHKDPRYSENDOIKWPWLMDEWSNEKSRL 690

Qy 644 LQRTGSPRVPQFGKQLOGSGAAGPRLFHIDANTNLPAHCTNRDIPPSY 703  
 Db 691 LQTTGSPRIPQGKQLOGSD--GPRKFTIEKA-GEPNKLUKAHTCFNRLDIPPSK 746

Qy 704 EKLYEKILTAVERTCGFAVE 723  
 Db 747 KOLDHKUSIAVETTIGFGQE 766

RESULT 5  
 US-09-070-060-4  
 Sequence 4, Application US/09070060  
 Patient No. 576849  
 GENERAL INFORMATION:  
 APPLICANT: Rustad, Carolyn M.  
 APPLICANT: Ghildayal, Namit  
 TITLE OF INVENTION: Human E3 Ubiquitin Protein  
 TITLE OF INVENTION: Ligase  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZEMECA Pharmaceuticals, Inc.  
 STREET: 1800 Concord Pike

CITY: Wilmington  
 STATE: DE  
 COUNTRY: USA  
 ZIP: 19850-5437

COMPUTER READABLE FORM:  
 MEDIUM TYPE: diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/070,060  
 FILING DATE: 30-APR-1998  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/073,839  
 REFERENCE/DOCKET NUMBER: PHM-70312

TELECOMMUNICATION INFORMATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Higgins, Patrick H  
 REGISTRATION NUMBER: 39,709  
 FILING DATE: 05-FEB-1998  
 TELEPHONE: 302.886.4889  
 TELEX: 302.886.8221

INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 854 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: Peptide

US-09-070-060-4

Query Match Score 33.9%; Length 854;  
 Best Local Similarity 35.4%; Pred. No. 1.1e-21; Mismatches 229; Indels 220; Gaps 29;

Matches 316; Conservative 108; Mismatches 229; Indels 220; Gaps 29;

Qy 6 KIRLVLCK-NLAKKDPFRLPDPFAKIVDGSGQCHSTDVTNNTDPKRNQHYDLYVG 64  
 Db 9 QLQITVISAKLKENKQWFG--PSPVETVDP--GQSKTKTEKONNTSPKWKQPLTVIP 65  
 Qy 108 --LDICKLKPSPDPAVKQGIVS-----LQFD--RIGTS--VVDCR 145  
 Db 123 GDLSVC-----LDGQVAAEVVNGTGETSESTQNDDGCCRDRDTRVSTNGSDEPVAAS 178  
 Qy 146 G-----LLENEGTIVYEDSGPGRPLSCFMEBAPY-----DSTG 179  
 Db 179 GENKRANGNNSPNSLNGG--FKPSRPRP----SRPPPTPRRPARNSPSTSNSDSDG 231  
 Qy 180 AA-----AGGGNCRPVPSQ-----DPLQAQR 203  
 Db 232 SSTSSLPPNTNTNTSTSGATSGLILPLTSSGSGPRLPLNTVSQPLPFWCERQY--- 287  
 Qy 204 LRNPDVRLG-----QTPQRPHGHQSPELPEGYEQRTVOQGVYIHLQTGTGSTM 255  
 Db 288 ---DQHGRVYVYDHVERTRTWRPE---SLPPGWERVYDNMGRIYTTDHTPTTITQ 338

Qy 256 DPRIP-----RDL---NSVNCDELGPPLPGWEVR 281  
 Db 333 RPTLSRVNVEQWQLQRSQLGAMQFNQRFYGNQDLEAFSQNKEFDPLGPPLPGWEVR 398  
 Qy 282 STVSRIFYFDHNRHTTQDTPRHLHMHOCQKERSQPL----- 324  
 Db 399 TDSNGKVIFNHNTRTQHBDPR---SQGQINE-KPREGEMRFTUDGIFYFVH 450  
 Qy 325 -----PSEGSLDEBLPAQRYERDVOQKLVIR--HBLSLQOPOQHCRERVS 372  
 Db 451 NRRATVYIDPRTGSKALDNGQIAYVDRFFAKVQIOFRFWCQOLAMQ---HIKITVTK 506



TELEPHONE: 302.886.4889  
 TELEX: 302.886.8221  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 852 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide

S-09-070-060-3

Query Match 33.5%; Score 1301; DB 2; Length 852;  
 Best Local Similarity 34.7%; Prcnt. No. 5.4e-120;  
 Matches 308; Conservative 126; Mismatches 241; Indels 212; Gaps 26;

Y 6 KIRLTVLCAK-NLAKKDFRLLPDPFAKIVDVGSSQCHSTDTVNTLDPKWQHNDLYRK 64  
 D 9 QLQITVYISAKLKTKENKG-PSPYVEVTVD-GQSKEKTERCNCNTNSPKWKQPLTVTTP 65

Y 65 TDSITISWVNHKKHHK - QGAGFLGVYVLLSNAISRLKDT-----GVQR-----L 108  
 D 66 VSKLHFRRVSHOTIJKSDVVLGTAADLYETLKSNNMKLVEVVTIQLGGSKKEPTETIGDL 125

Y 109 DLCKUNPSDDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144  
 D 126 SIC----LDGJQIOLSEVVNTGEITCSASASQNDGSRSKDETREVSTNGSDDPEDAAGEN 181

/ 145 RGL-----LENBGTVYEDSGPQRPLSCMFBAPYPTDSGAAGKGNCRFVES---- 192  
 > 182 RRVSGNNSPSLNSGG--FPSPSRPRP----SRPPIPPTPRAASPTGSATSES-DGSS 234

/ 193 -----PSQDQRLQAORLRNPD 208

) 235 GSLPPPTNTNTNTSEGATSGSLIIPITISGGSGRPLNPTQAPLPGWEMTRV-----D 286  
 ) 209 VRGSL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260  
 ) 287 QHGRVYYDVHDVERKPTWDEP-----PLPGWEMRVDNMGRYYDHFTRTTMQRPILE 341

/ 261 -----RDI-----NSVNCDEFGPLPGWEMTRV----- 342 SVRNTBQWLQLRSQLOGAMQFNQNRFTYGNQDLFATQSKEFDPGLPGWEMTRDNG 401  
 ) 287 RIYFVDHNNTTOFDPRLHHINMHCOLKEPSQPLP----- 324  
 ) 402 RVFVHNTTRTQWDPR-----SQGLINE--RPLPGWEMRFVTDGIPYFVHNRRT 453

) 325 ---PREGSLEDDELPFAQYERDVKQKLVR--HELSLOOPQAGHCRTEVSPEEIEE 377  
 ) 454 TYIDPRTGKSAALDNGQIAVVRDPAKQYFREWQOOLAMPQ--HKLTVTKTLEFD 509

) 378 SYROTMMRKPDKLKKRMLYKTFERGEGDUDGCGYARAEINTYLICHMLNPYXGLFCYSTDNY 437  
 ) 510 SFQIQMSFSPPDLRRLWTFPGEBGLDGGYAREWFLUSHEVINPMYCLFEAGKDRY 569

) 438 MLQINDSSINPDHSYEHVGRMLGLAVEHGHYINGCFPTVPPYKOLGKPIOLSDLSV 497  
 ) 570 CQINPASYNPDHKYFRTGIGRITANMFLHGPIDGFSLYFGRILNPKVGIRDLEI 629

) 498 DPELHKSLVNLLENDITPV-LDHTFCVBHNAFGRLKQHELKPNGRNVPTEENKEYVRL 556  
 ) 630 DEPFYNSLIWKENNIEECDELMFSVXEILGEEIKSHDLKPNGNLTVEENKEEYIRM 689

) 557 YNWWRPMRGIBAQFLALQKGFNEILIPOHLLKPSDQKBLELIGGLDKIDLNDWSNTLIK 616

) 690 VAEWRLRSGVEQTOAFFEFNEILPQCYLQYDKELEVILGCGQEIINDWORHAYR 749  
 ) 617 HCYADSNIURMFWMQAVETPDEERARLQOFVTSSTRYPLQGKALOGSTGAAGPFLPTH 676

) 750 HYARTSKQIMWFWQYKELINEXMRLLQFVTCRUPVGFADLNGSN--GPKFCIE 806

) 677 LIDANTDNLPAKAHTCFNRDIPPESYEKLYKLUTAVETCGFAVE 723

Db 807 KV-GRENLPLRSHTCFNRLDPPVSYEQUKRLFAEETEGQGE 852

RESULT 8  
 US-09-357-746-3  
 Sequence 3, Application US/09357746  
 Patent No. 608122  
 GENERAL INFORMATION  
 APPLICANT: ZENECA Limited  
 TITLE OF INVENTION: HUMAN E3 UBIQUITIN PROTEIN LIGASE  
 FILE REFERENCE: PHM 70312\_N1  
 CURRENT APPLICATION NUMBER: US/09/357,746  
 EARLIER FILING DATE: 1999-07-21  
 EARLIER APPLICATION NUMBER: US No. 60871222 60/073,839  
 EARLIER FILING DATE: 1998-02-05  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: PASESEQ FOR Windows Version 3.0  
 SEQ ID NO 3  
 LENGTH: 852  
 TYPE: PT  
 ORGANISM: Homo sapiens  
 US-09-357-746-3

Query Match 33.5%; Score 1301; DB 3; Length 852;  
 Best Local Similarity 34.7%; Prcnt. No. 5.4e-120;  
 Matches 308; Conservative 126; Mismatches 241; Indels 212; Gaps 26;

Y 6 KIRLTVLCAK-NLAKKDFRLLPDPFAKIVDVGSSQCHSTDTVNTLDPKWQHNDLYRK 64  
 D 9 QLQITVYISAKLKTKENKG-PSPYVEVTVD-GQSKEKTERCNCNTNSPKWKQPLTVTTP 65

Y 65 TDSITISWVNHKKHHK - QGAGFLGVYVLLSNAISRLKDT-----GVQR-----L 108  
 D 66 VSKLHFRRVSHOTIJKSDVVLGTAADLYETLKSNNMKLVEVVTIQLGGSKKEPTETIGDL 125

Y 109 DLCKUNPSDDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144  
 D 126 SIC----LDGJQIOLSEVVNTGEITCSASASQNDGSRSKDETREVSTNGSDDPEDAAGEN 181

Qy 145 TDSITISWVNHKKHHK - QGAGFLGVYVLLSNAISRLKDT-----GVQR-----L 108  
 D 66 VSKLHFRRVSHOTIJKSDVVLGTAADLYETLKSNNMKLVEVVTIQLGGSKKEPTETIGDL 125

Db 9 QLQITVYISAKLKTKENKG-PSPYVEVTVD--GOSKCTEKNCNTNSPKWKQPLTVTTP 65

Qy 146 KIRLTVLCAK-NLAKKDFRLLPDPFAKIVDVGSSQCHSTDTVNTLDPKWQHNDLYRK 64  
 D 9 QLQITVYISAKLKTKENKG-PSPYVEVTVD--GOSKCTEKNCNTNSPKWKQPLTVTTP 65

Qy 147 RGL-----LENBGTVYEDSGPQRPLSCMFBAPYPTDSGAAGKGNCRFVES---- 192  
 D 182 RRVSGNNSPSLNSGG--FPSPSRPRP----SRPPIPPTPRAASPTGSATSES-DGSS 234

Qy 148 -----PSQDQRLQAORLRNPD 208

Qy 149 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144  
 D 150 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144  
 Qy 151 -----PSQDQRLQAORLRNPD 208

Qy 152 SIC----LDGJQIOLSEVVNTGEITCSASASQNDGSRSKDETREVSTNGSDDPEDAAGEN 181

Qy 153 RGL-----LENBGTVYEDSGPQRPLSCMFBAPYPTDSGAAGKGNCRFVES---- 192  
 D 182 RRVSGNNSPSLNSGG--FPSPSRPRP----SRPPIPPTPRAASPTGSATSES-DGSS 234

Qy 154 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 155 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144  
 D 156 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144  
 Qy 157 RYFVHNTTRTQWDPR-----SQGLINE--RPLPGWEMRFVTDGIPYFVHNRRT 453

Qy 158 RYFVHNTTRTQWDPR-----SQGLINE--RPLPGWEMRFVTDGIPYFVHNRRT 453

Qy 159 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

Qy 160 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

Qy 161 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

Qy 162 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

Qy 163 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

Qy 164 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

Qy 165 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

Qy 166 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

Qy 167 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

Qy 168 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

Qy 169 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

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Qy 171 DICKLNPSDTDAVGQIVVSQTL-----RDRIGTGS-----VVDC 144

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Qy 312 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 313 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 314 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 315 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 316 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 317 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 318 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 319 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 320 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 321 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 322 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 323 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 324 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 325 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 326 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 327 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 328 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 329 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 330 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 331 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 332 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 333 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 334 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 335 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 336 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 337 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 338 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 339 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 340 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 341 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 342 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 343 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 344 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 345 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 346 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 347 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 348 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 349 VRSGL-----OPTQPQRPHGHQSPELPGEGYEQRTTVOQCVYFLHTQTGCVSTHDPRIP 260

Qy 35

RESULT 9  
 Sequence 6, Application US/08895601  
 Patent No. 606262  
 GENERAL INFORMATION:  
 APPLICANT: Beer-Romero, Peggy  
 APPLICANT: Strack, Peter J.  
 APPLICANT: Glass, Susan J.  
 APPLICANT: Rolfe, Mark  
 TITLE OF INVENTION: REGULATION OF KAPPA B (IKB) DEGRADATION,  
 NUMBER OF SEQUENCES: 16  
 ADDRESS/RECORDED ADDRESS:  
 FOLEY, HOAG & ELLIOT LLP  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109-2170  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 FILING NUMBER: US/08/895, 601  
 FILING DATE: 16-JUL-1997  
 CLASSIFICATION: 435  
 NAME: Vincent, Matthew P.  
 REGISTRATION NUMBER: 36,709  
 REFERENCE DOCKET NUMBER: MIV-096-01  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: 617-832-7000  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 927 amino acids  
 TYPE: amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 -08-95-601-6

Query Match Score 1259; DB 3; Length 927;  
 Best Local Similarity 33.6%; Pred No. 9,46-116;  
 Matches 307; Conservative 129; Mismatches 239; Indels 240; Gaps 28;

7 IRLTVLCAKNUAKDKEFLDRPEKAVV---VPGSGQCHSTDTVNTLDPKNN-----55  
 48 VRPRVIGIGLAKDGLGASPYRVRVLYDPNNVLTSVQTKTICKSLSNPKNNEBILFRV 107  
 56 ---QH---YDLYGKTD--SITISWN-----HKKHHKKQG 83  
 108 HPOQHRLLFVEVDENLRDDFLGQDVPLYPLTENPRLERFTFCDFLHPRSHKSRY 167

Qy 498 DPEHLKSLWILENDITPV-LDHTEFCVHNAGRILQHLPNKGPNRNVTEENKKEYVRL 556  
 Db 630 DPEFYNSSLINTKENNIEBCDLEMWYSDVKDEKSHDJKPNGNLIVTEENKEEVIRM 689  
 Qy 557 YVWRFRMFGIAEGLFLAQKGENLQFLQHLLKPFDKRELELIGLDKIDLNWKSNTRLK 616  
 Db 690 VAEPRLSRGVVECTQAFEGENEILQDQYLQYDAAKELEVLLCQEDLNWDQRBAIYR 749  
 2Y 617 RCVADSNIVRWMFOAVETDEERARLLQFTGSTRVPLQGFALQCGSTGAAGRFLFTH 676  
 Db 750 HYARTSKOIMWWPQFVBEIDERRARLLQFTGTRLPVGGFADLMSSN--GPQKFCIB 805  
 2Y 677 LIDANTDNPLKAHTCPNTRIDIPPEYSEKLYKEVLITAVETCGFAVE 723  
 Db 807 KV-GKENWLPRSHTCFNRLDLPKSYEQLKERKULLFAITEBTGGQEE 852  
 Qy 84 AGFLGCYRLLSNAILRKOT-----LCKL-----GXQRILD-----LCKL-----113  
 Db 168 KGYL-----RLKMTLYPKTSGSEDDNNEQAEBLEPGKVNVLQPDACHLQQQE 216  
 Qy 114 -----NPSD-TDAVRGQIVVSILQ---TRDR 134  
 Db 217 PSPLPPOWERQDILGRTYYVNHSRRTQWKRTPTQDNWLTDENGNIQLQRAFTRRQ 276  
 Qy 135 IGTGSVVDCEGFLG-----EGTYEDSG-PGRPSCMEMEPAYTD-----176  
 Db 277 ISBETESVDNOBSESNWEIREDATMYSQAPSPPSSNLDPVTHLAETLNARLTIFG 336  
 Qy 177 ---STGAAGAAGGNCR-----EVESPS-----ODORLQQRQL--204  
 Db 337 NSAVSOPASSNNHSSRRGSLQAYTFFEOPTLPVLLPTSSGLDPGWBEKQDRGGSYVDH 396  
 Qy 205 -----RNPHGHQSPELPGYEQ 234  
 Db 397 NSRTTWTKPVAQAVETSQLOSSQGQJASTSDGQQTQPSIEQGFLPKGWEV 456  
 Qy 235 RTTVQGQVYFLHTQGVSHTHDPK--IPRDINSV---NCDBLGPBPGBHEVYSTSGRI 288  
 Db 457 RHAPNRSPFEDHNTKTTWEDPLKPKPAHLRKTSLDTNSNPLGPBPGBHEBERTHDGRI 516  
 Qy 289 YFDVHNHNRTTOFTDPLRHLHMNTNOCOLKEPSQSLPLPSEGSLDEELPAQRYERDLYQKL 348  
 Db 517 FYTNENIKRQWEDERLYN----ATGPAYV-----YSRUYKRY 553  
 Qy 349 KUTRHESLQQOPOQACHCRLEVSREBIPFESTQIMQMRPKD-LKCRMLMVFKRGEGDYG 407  
 Db 554 EFRRKLUKQKCONDIPKFENKLRAVTLDSYRIMGYKRAFLKWLIEDGEGLDYG 613  
 Qy 408 GUAREMILYLCHEMNPYGLPQYQSTDNIMLQINPSSI-NPDHLSYFHVRGMRMLAV 466  
 Db 614 GWAREMFLLSKEMNPYGLPFEYSATONTYQINPNSGLCNEDHLSYFKRIGVAGMAV 673  
 Qy 467 FHGHYINGGTVPFKQKLGPQLSPLESVDPELHSLSWILENDITPVLDHPCVBNH 526  
 Db 674 YHGKLUDGEPTTRPFYKOMLHKPITLHOMESDVEYNSLRLTLENDPTBLDLRILIDEE 732  
 Qy 527 AFGRLQHELKPGNPNVPTEEENKEVYRLVNMWFRMIGEAQFLAQKGNEELPQHLL 586  
 Db 733 LFQGTOHELKNGGSEIVVNTNKKEYTYLQWRFYNRICKOMAKFEGFFELIPQDLL 792  
 Qy 587 KPDFQKELBLIGGDKDLDNRKSNTRLKH-CVADSNIVEWFWQAVETDEERARLLO 645  
 Db 793 KIFDENBLELMCGGIDVNDREHTKYKNGSYANHQVIONFWAVLMDSERGIRLQL 852  
 Qy 646 FVTGSPTRPLQGFKALQGSTGAAPRLTHTHIDANTDNPLKAHTCENRIDIPPESYEK 705  
 Db 853 FVTGSRVPMNGFELYGSN--GPQSETVEQW-GTPERKLPRAHICCFNRLDLPYTESFEE 908  
 Qy 706 LYEKLJLTAVETETCGF 720  
 Db 909 IWDKLQMAIENTQGF 923

RESULT 10  
 Sequence 6, Application US/08539205A  
 Sequence 6, Application US/08539205A  
 General Information:  
 Patent No. 6001619  
 General Information:  
 Applicant: Beach, David H.  
 Applicant: Caliguri, Maureen  
 Applicant: Nefsky, Bradley  
 Title of Invention: Ubiquitin ligases, and Uses Related Thereto  
 Number of Sequences: 6  
 Correspondence Address:  
 Addressee: Foley, Hoag & Eliot LLP  
 Street: One Post Office Square  
 City: Boston  
 State: MA  
 Country: USA

ZIP: 021-09-2170  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0., Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/539,205A  
 FILING DATE: 0-0CT-1995  
 NAME: Vincent, Matthew P.  
 AGENT INFORMATION:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 832-1000  
 TELEFAX: (617) 832-7000  
 INFORMATION FOR SEQ ID NO: 6:  
 CHARACTERISTICS:  
 LENGTH: 934 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 REFERENCE DOCUMENT NUMBER: CSV-005.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 832-1000  
 TELEFAX: (617) 832-7000  
 INFORMATION FOR SEQ ID NO: 6:  
 CHARACTERISTICS:  
 LENGTH: 934 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 08-539-205A-6

query	Match	Score	DR	Length	gaps
ISNAISL	31.6%	1228.5	3	834	
best Local Similarity	40.4%	Pred. No.	8.5e-113		
matches	276	Mismatches	211	Indels	93
244	1.35	IGTGGSVV-VDRCGLL--	-ENEGTVYEDSGPGRPLSCMEEAPYTTSTGAAGGON-	186	
246	1.36	LPSGWERRKDAGKRTYYVNHNRTTW-	--RPMQALAEDEGA--	134	-SGSATNSNNHL 295
187	1.37	CRFVESPQSDQRQLQAQRDNPDVGSL-	-----QPQNQRPHGOSPE	245	227
296	1.38	IEQQIRPRSLSSPTVTLASPLEGAKDSPYRRAVKTDLNPOSQSPSYNSPKPQHKVTQ	-----	355	355
228	1.39	-LPBEGVORTVQGVYFLHQTGVSTWDPRP-	--RDINSVANDDELQPPWEV	280	
356	1.40	SPPPGMEMTRAPNGRFPFDHNTKTTWDPRLKFPMRMSKTSLNNDGPLPPGWE	-----	415	
281	1.41	RSTVSGTIFYFDHNNTTGFTDPRLHIMNHQCQLKEPSQPLPLPSEGSLDEELPAQRY	-----	340	
416	1.42	RHLDGRTFYIHNSSKTQWDPRLON-----	--PATG-----	452	-PAPYI 452
341	1.43	ERDVLQKLVRLHELSLQQPAGHCRIEVSREEIFEBSYRQIMMM-RPKDLKLRMLKVKFR	-----	399	
453	1.44	SREKQKDYFRRKLKPADTFPNRFKMRNNTFEESTRRINSVRKRDVLKRLWFE	-----	512	512
400	1.45	GEEGLDDGGVAREWLILCHEMLNPXYGLFOYSTDNIVMLQINPDSSI-NPDHLSYHFV	-----	458	
513	1.46	SEKGDDGGVAREWFFLSEKEMNPYYGLPEYSATDNITLQINPNSGLQNEDEHLSYTFI	-----	572	572
459	1.47	GRIMGLAVPHFGHYINGGFTVPFYKQLLGPQIQLSLESTDPELHKSLMWLENDITVLD	-----	578	
573	1.48	GRVAGLAVPHFGKLLDFIRPYPKQMLGKQITLNDMEYSEYNSLNMWILENDITVLD	-----	631	631
519	1.49	HPCVENAFAGRLQHELKPGNRVPTTEENKEVYRLLVNWFMRGIBAQFLAQKGFN	-----	578	
632	1.50	LWFCIDENFGQTYQVNLKPGNSEMTVNENKREYIDLVIQKFNVRQKOMNAPLEGFT	-----	691	
579	1.51	ELLPQHHLKPPDKQKELELLIGLDKDNWKSNTRLKHCVADEBN-TRVWFGCAETFDE	-----	637	637
692	1.52	ELLPIDLIKIFDENELLMGGLGDVNDWROHSIYRONGYCPNHPVQWNKAVALMDA	-----	751	751
638	1.53	ERARLLOFVTSTRVLOGFAQLCSTGAGPRAFTIILIDANTDNPKAHTCFNRIIDI	-----	697	
752	1.54	ERKIRLLOFVTSTRVNGAELKSN--GPQLTIEFW-GSPKELPRAHTCFNRLDL	-----	807	807

b 453 SREFFQKYDFRKLIKKPADIPIRPFEMKLHRNNIIEEYRRIMSVRDPVLKARLWIEPE 512  
 y 400 GEEGDYGGYAREYLILLHEMADPYKELQFQISTDNYMLQINPDSOI-NPDHLSUHFV 458  
 b 513 SEKGKDGYGGYARENFFLISKEMFPPYGFYEFATDNYTQLQINPNSGLCNEBDHLSYFTFI 572  
 Y 459 GRINGLAFLVFGHHTYNGGFTVPPFKQLLGKPIOLSDLSAVDPLBLHSILUVWLBNDTTPVLD 518  
 b 573 GRVAGIAFLVFGKLLIDGFFTRPYKMLCKQITNDMSVSDEYNSLNUKWLBNDTTPB-LD 631  
 y 519 HTFCYEHNAFGRLQHELPKNGPVPTEENKEYVRLYNNWRFRGIEAOFLAQKGFN 578  
 b 632 LMPFCDDEENFGTQVLDLKPGNSIMVTNENKREYIDLVQIRFNRVQOMNAPLEGFT 691  
 Y 579 ELIPOELLKEFDQKBELELITGLKIDLNKSNTRLKHCVADSIN-TVRNFWOAYETFDE 637  
 b 692 ELLPDPLIKEFDENELELLMGCLGDDVNDWRHSTIKNGYCPNHPVIQWWKAWLMDA 751  
 Y 638 ERRABILQOFVGTSPVLOGFKAQGSTGAAGPRLFTHLIDANTDNLPKAHTCPRNIDI 697  
 b 752 EKRIRLQFVGTGSVAVPQNGFAEYGSN--GRQFLTIEQW-GSPELPRATHTCPRNIDL 807  
 Y 698 PPySEYKLYEKLLTAAVEETCGF 720  
 b 808 PPyTEFEDLREKLMAVENAQGF 830

ESUT12  
 S-08-630-916A-48  
 Sequence 48, Application US/08630916A  
 GENERAL INFORMATION:  
 APPLICANT: Pirozzi, Gregorio  
 APPLICANT: Kay, Brian K.  
 APPLICANT: Fowlkes, Dana M.  
 TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
 TITLE OF INVENTION: POLYPEPTIDES HAVING WWW DOMAINS AND METHODS OF USING SAME  
 NUMBER OF SEQUENCES: 124  
 CORRESPONDENCE ADDRESS:  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/630,916A  
 FILING DATE: 03-APR-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MISROCK, S. LESLIE  
 REGISTRATION NUMBER: 18,872  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 896-8864/9741  
 INFORMATION FOR SEQ ID NO: 48:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 906 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide

IS-08-630-916A-48  
 Best Local Similarity 31.5%; Score 1225; DB 3; Length 906;  
 Matches 281; Conservative 115; Nismatches 227; Index1 169; Gaps 19;

28 PFAKIVVDGSGQCHSTDVTKNTLDPKMQHY---DLVYGKTDSITISVWNHKKTHKKQG 83  
 QY 188 PRNGSALTDGS-QLPSRDSSCTAVAE-NRHQPBPSTNCFGRS-----RTHREISG 234  
 Db 84 AGFLGCYTRILLSNAISRLKDGYQRLDLCKLNPSDTDAVGQIVVSLQTRDR-IGTGGSV 141  
 QY 235 AS -----ARTPATGEOSGARSRRHROVKNSGHS 264  
 Db 142 VDGRGLNEGTYVED-----SGPRPLSOPMEE---PAPYDSTAAGGGN 186  
 QY 265 GLANGTYNDEPTTATDPEEPBSVGVTSPPASPLSVTPNENTTSPPAPAPAEQ-----317  
 QY 187 CRFVEPSQD-ORLOAQRLRNPDVRSLOTPQNRPHEQSPBPE-----230  
 QY 318 ---EBGSTSGTQQLPA-----AQAPDALPAGEQRELPNGRVYYVDBHNTKTT 363  
 Db 231 -----GYEORTTVQGQVYFLHTQGVSWHDPRIIPRDLN-----264  
 Db 364 WERPLPPGWEKRTDPRGRFTYVHDNTTRTQWQRTAETYVRYNEQWQSORNQLQCAMQHFS 423  
 QY 265 -----SYNCDCDLGPJPPGWVRSVTSVGRYFYDVRINRTRQTDFP-----304  
 Db 424 QRELYQFWASSTDHDPLGPJPPGWERQD-NGRYYVNVNTRTQWEDRTQSMNIQEPAI 482  
 QY 305 -----LHHLMNHQCQLKEPKSQPPLPSSEGSLEDELPAQYRVDLYQKLKVLR 352  
 Db 483 PPGWEMKCYTSEGVRYFDHNTTRTFKDPRPGFEGTQKGSPGAYDRSPRWKTHQFRLLC 542  
 QY 353 HELSLOOPQAGHCRIEVSRBIFIPESYQIIMPRPKD1KXRLMKVPRGEGBLDGYYVARE 412  
 Db 543 HSNAL---PSHVKSVSQRLFEEDSFQOIMMMRPyD1RRLYTMRGEGJUDYGTIARE 598  
 QY 413 WLYLICHEMNYYGLQYSTNDTMYLQINPDSINPDHASYFHVGRINGLAVFIGHTI 472  
 Db 599 WFELLSHEBVNMYCLPEYACKNNYCLQINPASSINPDILTYFRFGRPIAMALYHGKFI 658  
 QY 473 NGGFTVPFYKQOLGKRIQLSDLESYDPELKSLWYILEDNTIPV-LDHFPCVYRNAFGR 531  
 Db 659 DCGTFLPFYKRNLYNREPTLQESIDFEPINSWIKENNLÉEGGLELPQMEILSKY 718  
 QY 532 LOHELKGNGRATPVRENKEYVRLYNNWRFRGIEAOFALOKGFNELIPOHLLKPFQD 591  
 Db 719 TTHBLKGEGESRVTEENKEKSYMLTDWFRTRGVEEQTKAFLGFGNEVAPLEMTRYFDE 778  
 QY 592 KUEFLIGGLKLLDANKNTBLGHCVADSNTVYRNEWQAVETDEEBARLQYVTGST 651  
 Db 779 KEUBLMCGMQIDMSDWQKSTVYRHYTKNSKQIOWENQVKENDNEKRILQFVTGNC 838  
 QY 652 RVPLQGFKALQGSTGAGPRLFTIHIDANTDNLPKAHTCFNRFDRIPYPSYCELYEKLL 711  
 Db 839 RLFYGGPRAELICSN--GPQFCIDEVGKET-WLPRSHTCFNRLDLPPKSYEQREKLL 894  
 QY 712 TAVEETGFAVE 723  
 Db 895 YATEETEGSGQZ 905

RESULT 13  
 US-08-630-916A-46  
 Sequence 46, Application US/08630916A  
 Patent No. 6011137  
 GENERAL INFORMATION:  
 APPLICANT: Pirozzi, Gregorio  
 APPLICANT: Kay, Brian K.  
 APPLICANT: Fowlkes, Dana M.  
 TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
 TITLE OF INVENTION: POLYPEPTIDES HAVING WWW DOMAINS AND METHODS OF USING SAME  
 NUMBER OF SEQUENCES: 124  
 CORRESPONDENCE ADDRESS:

STATE: New York  
 COUNTRY: United States  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/630, 916A  
 FILING DATE: 03-APR-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MIRROCK, S. LESLIE  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 1101-203  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 896-8864/741  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 683 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 -08-030-916A-46

Query Match 27 0% Score 1047; DB 3; Length 683;  
 Best Local Similarity 43.8%; Pred. No. 6.9e-95;  
 Matches 217; Conservative 81; Mismatches 146; Indels 52; Gaps 10;

190 VSPSPQDORIQAQRNRPDVRSQI-----TPQNRPHQHOSPELPEGEQRT 236  
 225 MEISVRAFEQWOSQR--NOQUGMLOFNQDRYLSASMLAAENDPYG---PDPGWEKRV 277

237 TVQGQYFLHTQGTSTWDPRIDLNNSVNCDBLGLPLPPGMWVRSYSGRIVFDHNNR 296  
 278 DSTDRYFVNENTKTQWEDERTQGONE-----EPLPEGWIRYREGVRFVDENTR 331

297 TTQFDPRHLHMNTAQQLKEPSQLPLPBEGLSDEELPAQBYERDVLQKUKVRLHELS 356  
 332 TTFKQPR-----NGSSV-----TKGG-----PQIAYERFRWLKAHFRTY-LC 369

357 IQQPQAGHCRTEVRSEBTFEESSYRQIMKRPDKIKRMVKFRGEGLDYGGVARELYL 416  
 370 QSNALPHVKINVSQTLFEDSFQIQMALKPQDLRRLXVTFGEGLDYGGFARREFFL 429  
 417 LCHEMLNPYYGLFOYSTDTNTYMLQINPDSSTINPDILSYFHFGRIMGLAVFGHYINGGF 476  
 430 LSHEVNLNMYMCUFLFYAKNNYCLQINPASTINPDILSYFCFIGRIMALFHGKFIDTGF 489

477 TPFYKQOLLGKTIQSLPDESVDPEHKSLYWILENDITYP-LDFTCFEHNAFGRLOHE 535  
 490 SLPYKRMNLSKLTQKLESIDTFTNLSWIRDNNIEEGLENFSYDMEILGKTSHD 549

536 LKPNGRNTPYTBEENKEYKVRLYXVNWRMRGTEAQLAQKGENELIPQHLLKPFQDQKBLE 595  
 550 LKIGGSNLVYTNKDYIGMTERFSRGQEQKRAFLDGFENEVVPLQWLFDFECELE 609

556 LIIGGLDKIDLANDWKSTRKLHCVADSNIYVWMQAVETDEERRARLIQOFUTGSTRVPL 655  
 610 VMLCGMDEVLDADWQRTVYRTRSKOIIWFMQFKETDNEVTRMRLIQFVTGCRPL 669

656 QGPRAKQDQSTGAAFR 671  
 670 GGPFAELMSN--GPR 682

RESULT 14  
 08-247-904B-8 Sequence 8, Application US/08247904B  
 Patent No. 5981699

GENERAL INFORMATION:  
 APPLICANT: Role, Mark  
 ADDRESS: Foley, Hoag & Eliot  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII (text)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/247, 904B  
 FILING DATE: 23-MAY-1994  
 CLASSIFICATION: 510  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Vincent, Matthew P.  
 REGISTRATION NUMBER: 36,709  
 REFERENCE/DOCKET NUMBER: MIV-029.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 832-1000  
 TELEFAX: (617) 832-7000  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 874 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-247-904B-8

Query Match 13.7% Score 530.5; DB 2; Length 874;  
 Best Local Similarity 26.1%; Pred. No. 2.7e-43; Mismatches 262; Indels 159; Gaps 26;  
 Matches 190; Conservative 117; Mismatches 262; Indels 159; Gaps 26;

98 SRLKDTGYWORLDJCKLNPSDT----DAVRGQIVVLSQTDRIGTG-----GSVVDR 145  
 202 SRIDSSGQDNNNQKLGPDDYSVDDIAIR-RVYTRILSNEKIEATAFLNALVYLSPNVECD 260

146 GLLNEGTYV-----E-----DSDSPGPRPLSCFMEPAPYTDGCAAG 183  
 261 LTVEN--VYSRDPNVLNLFIGMENRNLHSPEYLEMALPFLCKAMSKLPL-----LAAQ 311  
 184 GGNCRFVESPSSQD-----R-----RLQRQLRNPD-----R-----R-----  
 312 GKFLRLWSKYNAQIIRRMMETIQQLITYKVISNEFNSRNLYNVEDNSRNLYDDAIVAS 3771

209 -----VRSLSQTQNRFRGHQS-PELPE-----GYPEQTTVQGQVYFLHTQT 249  
 372 KCLRMVYTAVNGGEVDTNHNEEDDEBTPESSELTQELIGERENKKGLRVDPDLETEL 431

250 GVST-----WHDRPRD-LNSVNCDELGPLPPGMWVRSYSGRIVFDHNNRTTOFDPLR 305  
 432 GVKTLDCCRPLREPLPEEFINE-----PLNEYLEMDDYTF-KPFI 482

306 HHHMHQCOLKEPSQPLPSESSLEDEELPAQRYERDVLQKLVRLHELSLQQPOAGHC 365  
 483 LNATVKNLGHYDNR-TMYSE-----RRITVL-YSLVQGQZNPYL 522

366 RIEVSRETFEES--YRQIMKRPDKLQKLMKFRGEGLDYGGYAREMLYLCHEML 422  
 523 RLKVRDHLIDDALVRLMEMAMENPDLKQLYVEFGEOQDGVSVKSFOLVYEEIF 582

423 NPYYGLFOYSTDNYMLQINPDSINPDHLSYFVRIGLAVFHIGYINGGFTVPPYK 482  
 583 NPDMGMPYD-ESTKLFWNPSSF--ETEGQFTLIGIVLGIAYNNCILDVHFPMVYR 638 B

483 QLLGKTEQLSPLESTDPELKSLWYILE--NDITPVLDDHTFCV-EHNAAGRILQHHLKPN 539  
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 639 KLMGKGGLFLGDGHPLVYQSLKELLEPGNVEDDMITFQISQTNLFGNMMLKRN 698  
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 540 GRNVPTTEENKEYRLLTQNWRMFGIEAQFLAQGF---NELIPOHLLKPFDEKELE 595  
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 699 GDKPTTNEKRFKFLNDSYDILANKSVENOFKAERGHFMVTNESPLKLFRP---EEIE 755  
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 596 LIGGDKIDLNDWKSNTLK-HCVADSNIVRNEWQAVETFDEERRARLUOFVTGSTRVP 654  
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 756 LLICGERNLNQDQALBETTEYDGTRDSVLIREWEWIVHSFIDBQRRLFLQTTGDRAP 815  
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 655 LGKFKAQGSTGAASGPRLFTIHLIDANTDNLPKAHTCENRIDIPPSYEKLYEKULATAV 714  
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 816 VGGIAGKMIATKNGSP-----DTERLPLSTTCENVILLPEYESKEKLKERLKA 865  
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 715 BETCGAV 722  
 :|:  
 866 TYAKGRCM 873

SULT 15 -08-76-7-942A-21  
 Sequence 21, Application US/08767942A  
 General Information:  
 APPLICANT: Rolfe, Mark  
 APPLICANT: Chiu, M. Isabel  
 APPLICANT: Berlin, Vivian  
 APPLICANT: Damagnez, Veronique  
 APPLICANT: Dreatta, Giillaume, Cottarel  
 TITLE OF INVENTION: UBAQUITIN CONJUGATING ENZYMES  
 NUMBER OF SEQUENCES: 45  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109-5170  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 REFERENCE/DOCKET NUMBER: US/08/767,942A  
 TELECOMMUNICATION INFORMATION:  
 FILING DATE: 17-DEC-1996  
 TELEPHONE: 617-832-1000  
 TELEFAX: 617-832-7000  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 NAME: Vincent, Matthew P.  
 REGISTRATION NUMBER: 36,709  
 REFERENCE/DOCKET NUMBER: MIV-029.04  
 TELECOMMUNICATION INFORMATION:  
 FILING DATE: 17-DEC-1996  
 TELEPHONE: 617-832-1000  
 TELEFAX: 617-832-7000  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 874 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 -08-767-942A-21

Query Match 13.7%; Score 530.5; DB 3; Length 874;  
 Best Local Similarity 26.1%; Fred. No. 2.7e-43;  
 Matches 190; Conservative 117; Mismatches 262; Index 159; Gaps 26;  
 98 SRLKDCTYQRLDLCLNPSDT---DAVRQCIVVSLQFRDRIGT-----GSVYDCR 145  
 202 SRIGGSQGDNLQKQGPDDVSVDADIR-RVYRFLSEKETAFNALVIVLSANECD 260  
 146 GLLNESTVY-----EDSGPGRPLSCFMEEBAPYTDSTGAAAG 183

Search completed: February 20, 2004, 15:36:25  
 Job time : 20.2366 secs



SULT 2 -10-021-660-81 Sequence 81, Application US/10021660  
 Publication No. US20030152926A1  
 GENERAL INFORMATION:  
 APPLICANT: Murray, Richard  
 APPLICANT: Glynn, Richard  
 APPLICANT: Watson, Susan R.  
 APPLICANT: EOS Biotechnology, Inc.  
 TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis, Compositions and Methods of Screening for Angiogenesis  
 TITLE OF INVENTION: Modulators  
 FILE REFERENCE: 018501-000710US  
 CURRENT APPLICATION NUMBER: US/10/021,660  
 CURRENT FILING DATE: 2001-12-06  
 PRIOR APPLICATION NUMBER: US/09/784,356  
 PRIOR FILING DATE: 2001-02-14  
 PRIORITY NUMBER: US 09/637,977  
 NUMBER OF SEQ ID NOS: 135  
 SEQ ID NO: 81  
 LENGTH: 748  
 ORGANISM: Homo sapiens  
 -10-021-660-81

---

61 VGTIDITISVWNHKKHHKQAGFLGCYRLLSNAISRLKDCKLNPSDTCV 120  
 122 AGQIVNSLQRDRIGGSIWDCRLLNEGTVEDS3PGRPLSCMHEEPAVTGAA 181  
 121 RGQIVNSLQRDRIGGSIWDCRLLNEGTVEDS3PGRPLSCMHEEPAVTGAA 180  
 182 AGGGNCRFVESSPSQQLQOQLRQLANPDQSLQPQNQPHGHOSPELPEGNEQRTVQQ 241  
 181 AGGGNCREVESSPSQQLQOQLRQLANPDQSLQPQNQPHGHOSPELPEGNEQRTVQQ 240  
 242 VYFLHTQTGYSTWHDPRIPRDLSVNCDELGPQPGMVERSTSGRTYFVDENNRQTFT 301  
 241 VYFLHTQTGYSTWHDPRIPRDLSVNCDELGPQPGMVERSTSGRTYFVDENNRQTFT 300  
 302 DPLRHIMNHOCOLKEPSOPLPSEGSLDEELPAQYERD1VOKLVRLHELS1QOPO 361  
 301 DPLRHIMNEOCQLIPEPSQQLPSEGSLDEELPAQYERD1VQKLVRLHELS1QOPO 360  
 421 LNPYGLFOYSTNDIYMLQINPDSSEINPDHLSKFHYGRINGLAVFHGHYINGFVPPF 481  
 482 KQLLGKPIQSLDLEVDPELHKSLWILENDIPLDHTFCVBNHAGRIQHELPNGR 541  
 481 KQLLGKPIQSLDLEVDPELHKSLWILENDIPLDHTFCVBNHAGRIQHELPNGR 540  
 542 NVPVTEENKEYVRLUVNPFMRGTEAQPLAQKFNLIPOLLRFDQKEBLELIGGL 601  
 541 NVPVTEENKEYVRLUVNPFMRGTEAQPLAQKFNLIPOLLRFDQKEBLELIGGL 600  
 602 DRIDNDWKSNTRLHCYADSNITRWNOAVETDEERARLQFYTGSTRVPLQFKAL 661  
 601 DRIDNDWKSNTRLHCYADSNITRWNOAVETDEERARLQFYTGSTRVPLQFKAL 660  
 662 QGSTGAAGPRLFTHLIDANTDNLPKAHTCENRIDIPYESYEKLTKAVEETCGFA 721  
 661 QGSTGAAGPRLFTHLIDANTDNLPKAHTCFNRIDIPYESYEKLTKAVEETCGFA 720  
 722 VB 723  
 721 VE 722  
 707 WIENDITPVLDITPVLDITPVLDPELHKSLWILENDIPLDHTFCVBNHAGRIQHELPNGR 534  
 535 WIENDITGVLDITGVLDITGVLDPELHKSLWILENDIPLDHTFCVBNHAGRIQHELPNGR 534  
 567 BAEFLAQKGKNELIPOHLLKPKEDQKELLELIGGDKDNDKSNTPLKHCYADSNITVR 626  
 595 EAFLAQKGKNEVIPOHLLKPKEDQKELLELIGGDKDNDKSNTPLKHCYADSNITVR 626  
 627 WPNQAVETDERRARLQFTGSTRVPLQFKALQNGPNTLKHCTPDSNTVK 654  
 655 WPNQAVETDERRARLQFTGSTRVPLQFKALQNGPNTLKHCTPDSNTVK 654  
 687 KAHTCFNRIDIPYESYEKLTKAVEETCGFAVE 723  
 712 KAHTCFNRIDIPYESYEKLTKAVEETCGFAVE 748  
 RESULT 3  
 US-10-313-955-2  
 / Sequence 2, Application US/10313955  
 / Publication No. US2003019036A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Beach, David H.  
 / CALIGURI, Maureen  
 / NEFSKY, Bradley  
 / TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto  
 / NUMBER OF SEQUENCES: 6  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: FOLEY, HONG & ELIOT LLP  
 / STREET: One Post Office Square  
 / CITY: Boston  
 / STATE: MA

COUNTRY: USA  
 ZIP: 02109-2170  
 COMPUTER READABLE FORM:  
 MEDIUM: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/313,955  
 FILING DATE: 05-Dec-2002  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/09/392,163  
 FILING DATE: <Unknown>  
 NUMBER: 08/539,205  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Vincent, Matthew P.  
 REGISTRATION NUMBER: 36,709  
 REFERENCE/DOCKET NUMBER: CSV-005.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 832-1000  
 TELEFAX: (617) 832-7000  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 735 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
  
 -10-313-955-2

Query Match 75.0%; Score 2913.5; DB 12; Length 735;  
 33st Local Similarity 72.9%; Pred. No. 6.2e-258; Gaps 9;  
 Matches 55; Conservative 63; Mismatches 71; Indels 18;

5 IKIRILTVLCAKNAKKDFRLLPPPAKAKVVDSSGQCHSTDTVKNTLDPKRNQHDLVYSGK 64  
 12 VKEVLIT-----GLPDPFAKVVDSSGQCHSTDTVKNTLDPKRNQHDLVYKGK 58

65 TDSTITISWVNHKCITHKQGAGFLGCVRLSNASIRLKDGTGYRLDICKNPSDTDAVRQQ 124  
 59 SDSVTISWVNHKCITHKQGAGFLGCVRLSVAIRLKDGTGYRLDICKLGPNNDNTVRQQ 118

125 IIVSLQLQRDRIGTGTGGSYVDCRGLLENE-----GTVY----- 155  
 119 IIVSLQSRDRIGTGQVYDCSRFLPDGMBERRTASGRIQYLNHITRTTQWRPRP 178

156 --EDSGPGPLSFMEBEPAPYDPISTGAAAGGGNCRVEFSDQDQLQAQLRNPDVRSGL 213  
 179 ASESSSGPLSCVTDENTPISTGNGATCG-----QESDPPLAERVRQRHNTM 229

214 QTPQNRPHGOSPHSPPLPEGYFQRTTVQOQYFLHTQGVSTHDPRIPLDINSNCDEGP 273  
 230 ---SRTHLHPTDPLPEXYFQRTTQOQYFLHTQGVSTHDPVPRDLSNINCEELGP 285

274 LPPPMWEVSTVSGRIFTYDHNRTTQTDPR---LHHINHOCOKEPSQPLLPSPSGS 329  
 286 LPPGWEIRNTATGRVYFVDHNRTTQTDPLSANLHLVLRNQKLDDQQQVW---S 341

330 L---EDEELPAQRYERDLVQKLKVRLHELSLQOPOAQCRCIYEVSREEIFPESYRQIMCR 386  
 342 LCPDDTELTIVPYYKRDIVQKLRLBELSOOPQGQHCRIEVSSEEIIBESTRQVMMR 401

387 PKDLIKRKLMKFPRGEGLDGYYGAREWLYLCHEMNPYGLFOYSTDNIYMLQINPDS 446  
 402 PKDLIKRKLMKFPRGEGLDGYYGAREWLYLCHEMNPYGLFOYSRDIYTQINPSA 461

447 INPDFHLSYPFHGRIMGLAVFGIHYINGGFTVPFKQOLKAPIQIQLSLESVDPHLKSLV 506  
 462 VNPEHLSYPFHGRIMMAVFGIHYIDGFFKQOLGSKITLDMELVDPHLNSLV 521

507 WIENDITPVLDTIPVLDLTCYHAFGRILQHELXPNGRNVPTEENKEYRLYNNWRMFGI 566

SULT 5  
-10-313-355-4  
Sequence 4, Application US/10313955  
Publication No. US2003019936A1  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
Caliguri, Maureen  
Neffay, Bradley  
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/313,955  
FILING DATE: 05-Dec-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/392,163  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/539,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: CSV-005.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1000  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 766 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
MOLECULE TYPE: Protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
-10-313-355-4

Query Match Score 1471; DB 12; Length 766;  
Best Local Similarity 40.9%; Pred. No. 1.6e-125; Indels 235; Gaps 20;  
Matches 327; Conservative 118; Mismatches 233;

) 4 SIKIRUTIVCAKNLAKKDFPRLPDPFAKIVDGGCHSSTDVTKNTDPKNNQHYDLYVG 63  
7 SRRITRTVAADGLYCRDVERPFDPAVITVDGE-QHTTTTAKKTNPYNNETFEVNT 65

) 64 KTDSTISITSWNHKKHKKQGAGFLGCCVRLLSNA-TSLRUDTYQQL--DLCKUNPSDDAV 121  
66 DNSTIAIQVFQKKP-KKKGGFLGVINLRVGVDLAIQGDEMILTRDLSKSN - ENTUV 122

) 1.22 RGQRWVLQ-----TRDRIGTGGSVVDCRGLLENEGTYYED 157  
1.23 HGKILINUSTAQSTLQVPSSAAASGARTQTSITNDPQSSKSSVRNPASSRAGSPTRD 182

) 158 SGPG-----RPSCFMEE-----PAPY--TGTG-----AAA 182  
1.83 NAPAAPASSEPRTPRSSFEDYGRIPGHEERRTSTWTRPNLSVA 242

) 183 GGGNCNCFVEPS-----QDQRLOAQRLRNPDYRGSIQTPQNRPHQSPELPECYQ 234

) 243 GAAAEDHSSAASSANTVEGQPSSSNAARTEA-SVLTNSATTAG----SCBLLPPEWQ 296

) 235 RTTVQGQVYELHTQTGVSTWDPRIPRDLNSVN-----CDELGPLPPGWVRST 283

Db 297 RYPPEGRPFYVDHNTRTTTWDPQQYIBSYGGPNNATIQQQPVSQLGPLPSQWEWRLT 356

Qy 284 VSGRIYFVDHNTRTTQFTDPRLHIMNHQCOLKEPSQPLPSSGSLDEBEPQRYERD 343

Db 357 NTFRVYFDENTKTTWDPR-----LPS -SL-DQNPV -QYRDR 392

Qy 344 LYOKLKVLRHESLQOAGHRTEYESREELFEESYRQIMKMRPKDLCRMLYKFRGREG 403

Db 393 FRKLIVFLSQLP-HLPGQHIIKVRNNHFEDSYAEINRQSATDLKRLMKFDGEG 451

Qy 404 LDYGGVAREWLYLCHEMLNPDYYGLFOYSTNDNIMLQINPDSSTINPDHUSYFHVGrim 463

Db 452 LDYGLLSREYFFLSHEMFNPFYCPEYSSVNTLQINPHSGINPEHNYFKTIGRVIG 511

Qy 464 LAFFGHYINGSETVPPYKQOLGKPQLSDLESVPELKSLVWILENDITPVLHDHFCV 523

Db 512 LAFFHRRFVDAPPVVSFKMLQKKTQLODMSDAEYXRSLVLTLDNITGVQDLTFEV 571.

Qy 524 EHNAFGRLQHELPKPNERNVPTEENKEYVRLYNNWRFMRGIAEQFLAQKGPNELLFQ 583

Db 572 EDRCFGETVTTIKLPGNRNIEVTEENKEYVRLYNNWRFMRGIAEQFLAQKGPNELLFQ 630

Qy 584 HLLKPFDEKELIJIIGGLDKIDLNDSKNTLKHCVADSNIVRNFWQAVENTFDEBERRNL 643

Db 631 ELLNVEDERELELLIGGISEIDMEDMKKHDYRSYSSENOLIKFWELMDEWSBKKSRL 690

Qy 644 LQFTTGSTRVPLGFXALQGSSTGAASPRLFTHIDANTNLPKAHTCNRIDLPPYEST 703

Db 691 LQFTTGSTRIPNGFKQLQGSD---GPKFTEKA-GEPNKLPKAHTCFNRIDLPPYTSK 746

Qy 704 EKUYEKLTATAVETCTGFAVE 723

Db 747 KDLDHKLSTAVENTTGFQE 76

RESULT 6  
US-10-032-585-7296  
; Sequence 7296, Application US/10032585  
; Publication No. US2003018095A1  
; GENERAL INFORMATION:  
; APPLICANT: Terry, Roemer D.  
; APPLICANT: Bo, Jiang  
; APPLICANT: Charles, Boone  
; APPLICANT: Howard, Bussey  
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery  
; FILE REFERENCE: 10182-005-939  
; CURRENT APPLICATION NUMBER: US/10/032,585  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 8000  
; SEQ ID NO: 7296  
; LENGTH: 932  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-10-032-585-7296

Query Match Score 1436.5; DB 12; Length 832;  
Best Local Similarity 38.4%; Pred. No. 2.6e-122;  
Matches 326; Conservative 124; Mismatches 233; Indels 167; Gaps 21;

) Qy 7 IRLTVLCAKNTLAKKDFFRPLPDPFAKIVDGGCHSSTDVTKNTDPKNNQHYDLYVGKTD 66  
Db 17 INVRVAEESLYKDRVERQPDFAVITVDGS-QTKTITAKTKTPYNNETFN-FQAKED 74

) Qy 67 SI-TISWNHKKHKKQGAGFLGCVRL-ISNAISRLKDTGYQL - DICKLNPSDTCAY 122

) Db 75 SILVIVQEDQKER-KKKDQGFLGVINVRGHDVILSNSSEETTRDLKSN - ENLVAIS 131

) Qy 123 GQIVYSLQ-----TRD-----RIGTGSVWTCRGLLE 149

) Db 132 GKIVVISHNRSNGGVTATTGTGASSNNIATITSGVNNRIGSATATTANISTAQS 191



ISULT 8  
3-10-097-534-15Sequence 15, Application US/10097534  
Publication No. US20030049607A1

GENERAL INFORMATION:

APPLICANT: GREENBER, TSVIKA

APPLICANT: MOSKOWITZ, HAIM

APPLICANT: REISS, YUVAL

APPLICANT: AROY, IRIT

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL  
TITLE OF INVENTION: MATURATION

FILE REFERENCE: PIV-001-01

CURRENT APPLICATION NUMBER: US/10/097,534

CURRENT FILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: 60/275,224

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: 60/308,958

PRIOR FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: 60/340,170

PRIOR FILING DATE: 2001-12-07

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 15

LENGTH: 927

TYPE: PRT

ORGANISM: Homo sapiens

-10-097-534-15

Query Match 32 4%; Score 1259; DB 15; Length 927;

Best Local Similarity 33.6%; Pred. No. 6.1e-106; Mismatches 239; Indels 240; Gaps 28;

Matches 307; Conservative 129; MisMatches 239;

Match 7 IRLTIVLCAKNUAKKDFERLDPFAKIV--VDGSGQCHSTDTPVNLDPXN-----55

Match 48 VRVRVAGIGLAKDILGASPDYVTRVLTDPMANVLTSTQTKTSLNPKXNEELFRV 107

Match 56 --OH-----YDLYVGKD-SITISIVWN-----HRKIRHKQG 83

Match 108 HFQQRHLLFVEYFDENRLTRDGLDVPLPTENPLRLEYTFDDEVLPHSRSRV 167

Match 84 AGFIGCVLISNAISPLKDT----GYQRLD---LKCL-----113

Match 168 KGYL-----RLKNTYLPKTSGSDDDNAEQAEELEPGMWVLDQDACHLQQQE 216

Match 114 -----NSD--TDAVRGQVVSLO---TRDR 134

Match 217 PSPLPGWEEBRODILGRTYYNNHERRTQWRKTPQDNLTDAGNTQLQACRAFTRRQ 276

Match 135 IGTGGSVVDRCGLLEN-----EGCTVEDSG-PGRPLSCFMWEPAPTYD-----176

Match 277 ISEETTSVNDESSSNWEIREDETMISQATPSSPPSSNLDVPTHLAEINARATIFG 336

Match 177 ----SIGAAAGGGNCR-----EVESBS-----

Match 217 NSAVSQDAPPNNHSSRGSQLQAYTEEQPTLPVILLPTSSGLPGEWWRGRSYVDH 396

Match 205 -----RNIDYRGSQLQTPQ-----NRPHGHQSDELPFGYEQ 234

Match 397 NSRTTWTKEPVQAVTEISOLTSSQASSAGPOSQASTSDSGQOYTQPSIEQFLPQWEV 456

Match 235 RTTVQCGQVFLHTQGVSTWHDPR--IPDLSV-----NCDELGPLPQGWERTSTYSGRI 288

Match 457 RHAQNRPFFIDHNTKTWEDPLKIPAHLRGKTSLSTSNVLGPBPQGWERTHDGRI 516

Match 289 YFVDHNRTQFTDRLHHMNHQQLKEPSQPLPSEGSLDEELPAQYERDLYQKL 348

Match 517 FYINTNIKRWQEDRLENV---AATGPAV-----YSRDWKRKY 553

Match 349 KVLRHEBSLQOQASHCRIEVSREEIFFEFSYROMKWRPKD-LKXRMVKFRGEBSLDYG 407

Match 554 EFPRLKQKNDIPKFEMKLRRATVLEDSYRRIMGVRADEFJKARLWIEFDGERSLDYG 613

RESULT 9  
US-10-205-823-279

Sequence 279, Application US/10205823

Publication No. US20030108965A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John E.

APPLICANT: Endge, Wilson O.

APPLICANT: Ganavarapu, Marjula

APPLICANT: Gorbatcheva, Bella

APPLICANT: Hoersch, Sebastian

APPLICANT: Kamatkar, Shubhangi

APPLICANT: Wensey, Angelia M.

APPLICANT: Glatt, Karen

APPLICANT: Zhao, Xumei

APPLICANT: Anderson, Dustin

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

THERAPY OF PROSTATE CANCER

FILE REFERENCE: MR2-044

CURRENT APPLICATION NUMBER: US/10/205,823

CURRENT FILING DATE: 2002-07-25

PRIOR APPLICATION NUMBER: 60/307,982

PRIOR FILING DATE: 2001-07-05

PRIOR APPLICATION NUMBER: 60/314,356

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/325,020

PRIOR FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 60/341,746

PRIOR FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: 60/362,158

PRIOR FILING DATE: 2002-03-15

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 279

TYPE: PRT

ORGANISM: Homo sapiens

US-10-205-823-279

Query Match 32.2%; Score 1249.5; DB 15; Length 911;

Best Local Similarity 34.5%; Pred. No. 4.4e-105;

Matches 303; Conservative 120; Mismatches 243; Indels 211; Gaps 24;

Match 17 LAKDKFRIP--DPARI--VWDQSGKQH--STDIVNTNLKPNWHDLYVGKTD-S 67

Match 69 LPDSDELFLPQICDPVYKLSLYVADENRELAVQTKTIKTLNPKWNEEFYFVNPSNHR 128

68 ITISVNNHKKIKKQGAGFGCVRLISNAI-----SRLKDT 103  
 129 LLFVFENRTRD--FLQVDPBLSHIPEDDTMERMPTYKDFLRPRSHKSVRK-- 183  
 104 GYORLCLKNPSDTDAVRGQIVVSLQTRDRIGTSVHDRCG----- 146  
 184 GFURLKAYMPNG---GDEEENDSDQRDDMERGHWEVYDSNDSAQSQQEELPPPLPPG 238  
 147 ---LLENEGTY-----ED 157  
 239 WEEKVDNLGRTYVHNINRRTQWHRPSLMDVSSEDDNNIRQINQEAHRRFSRRHISED 298  
 158 SEP-----GRPLSCFMEEPAPEPDTSQAA----AGGGNCRFVESPQSD----- 196  
 299 LEPEPSISGGDVEPWETTISEEVNIGDSLGLAPPPASPGSRSTSPOLESELRSRLOQT 358  
 197 -----ORLQARQLRN-----PDVRCGSLQPQN 218  
 359 PDSNGEQFSSLIQRPESSRLRSCSYTDAEAQGHILPPGAKDSPVRAVKDTLSNPQSQP 418  
 219 RPHGHQPE-----LPEGEBQRTVQCGYYFHTQTSYSTHDPRIP-----RDINSV 266  
 419 SPNSSPKPKHQVKTQSFLPPGDEMRAPNGPFFDQNTKTITWEDPRKEPVHMRSKTSL 478  
 267 NCDELGLPPIPGEVRSVSGRIYFDVHANNETTOFDPRLEHHINHHOCQLKEPSQQLPLPS 326  
 479 NNDLGIPPPNEERHLDGRTFYDHNSCTIQEDPRLQN-----PA 521  
 327 EGSLEDEBLLPAQYERDLYVQKLKVLKRLHELSLQQPAGHRCIEVSREEFEESYRQIMKM- 385  
 522 ITG-----PAVPSRFKQXIDYRKKLKPADIPNRFEMKLHRNNFEESYRMLMSVK 575  
 386 RPKDLKRLMKYFRGEGCLDGGVAREWLILCHEMLNPFYQFQISDNINFLQINPDS 445  
 576 RDVVLKARLWTFEESEKGLDGGVAREWFLLSMEMENYYGLFEYSATDNYLQINPNS 635  
 446 ST-NPDEILSYRFVGRGIMGLAVPHHYINGGFTVYKOLGKPIQLSDLESYDPELHKs 504  
 636 GLCNEBHISYTFIGVAGLAVERHGSKLDOFFIREPYAMGLGQTINDMESYDSEYRNS 695  
 505 LYWLLENDITPVLDHTFCVVAENAFGRILQHELKGPNRGAPEVBNKEYVRLYVNWFMR 564  
 696 LXWLLENDPTLDLMFCIDBENFGTQYDVLKENGSEMVVNENKREXIDLVQRFVN 754  
 565 GREAQFLAQKGFENLIPOHUJKPDKELIELIGKDIIDNWKSNTRLHCVADSN- 623  
 755 RVQKQNAFLLEGTEFLPIDIKIDTENEELMGGLDVTNDWRQHSIYKNGYCPNHP 814  
 624 IVRWNOAVERFDEERRARLQFVTGSTRYPLQOGFKALOGSTGAAGPRLFTHLIDANTD 683  
 815 VIQWFWCAVLMDAERIRLQFVTGSTRPMNFAEYGSN--GPOLFTBOW-GSPE 870  
 684 NLPKAATCFCNRIDPPIYESKLYKLLTAVEETCGF 720  
 871 KLPRAATCFCNRIDLPPYETFDLRBKLMNAVFNQGF 907  
 SULT 10 -10-374-979-89  
 Sequence 89, Application US/10374979  
 GENERAL INFORMATION:  
 APPLICANT: John P. Carulli et al.  
 TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3  
 FILE REFERENCE: 032796-021  
 CURRENT APPLICATION NUMBER: US/10/374,979  
 PRIOR FILING DATE: 2003-03-04  
 PRIOR APPLICATION NUMBER: US 09/544,398  
 PRIOR FILING DATE: 2000-04-05  
 PRIOR APPLICATION NUMBER: US 09/543,771  
 PRIOR FILING DATE: 2000-04-05  
 PRIOR APPLICATION NUMBER: US 09/229,319

PRIOR FILING DATE: 1999-01-13  
 PRIOR APPLICATION NUMBER: US 60/071,449  
 PRIOR FILING DATE: 1998-01-13  
 PRIOR APPLICATION NUMBER: US 60/105,511  
 NUMBER OF SEQ ID NOS: 109  
 LENGTH: 739  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-374-979-89  
 Query Match 32.1%; Score 1245.5; DB 12; Length 739;  
 Best Local Similarity 39.8%; Pred. No. 7.3e-105;  
 Matches 274; Conservative 99; Mismatches 180; Indels 135; Gaps 18;  
 Qy 114 NPSTDIDAVRGQIVTIVSL-----QTRDRIG-TGSSVVDCRGLLENEGVYEDSGPGRPLSCF 167  
 Db 109 SPATSSESDGSSSTGSLPPPTNTNTNTSGATSLIPL-----TISGSSGP-RPLNPFV 159  
 Qy 168 MEERAPYDSTGAAAGGGNCRFVESPQSDORLQAORLNPDVYRGS-----OTPONR 219  
 Db 160 TQALP-----PWEQRL-----DQHGRYYVDHVEKRTTWDR 192  
 Qy 220 PHGQSPPELPEGYEORTTIVQGOVYFLHTQTCGVSTWDPRIP----- 260  
 Db 193 PE-----PDPGVERRDNMGHYYDHFTRTTWOPTLSVRYNEQWOLQRSQLQGAM 247  
 Qy 261 -----RDL---NSYNCDELQPLPPWEVRSVSGRIYFVDFHANRRTTQFTDPRU 305  
 Db 248 QFENQRFITYGNQOLFATQSXKBDFPLQPLPPWKRTDNSGRVYFHANRRTIWEDPR- 306  
 Qy 306 HHINHQCQLEKBDQPL-----PSEGSLDEDBELPAQR 339  
 Db 307 -----SOCQLINE-KELPPEGWMRFTYDGIPIFYDHNRRRTTYDERTGKSALDNGPQIA 359  
 Qy 340 YERDLVQKLVLR-----HELSLOOPQASHCRLEVSRERI FEESYRQJIMKNEPKDILCKRLMV 396  
 Db 360 YVRPKARYQYFERWCQOLAMQ---HIKITVTRKTLFEDSFQQIMSFSQDQRLRLWV 415  
 Qy 397 KFREGBGLDGGTAREWLYLCEMINPYYGLFOYQSTDNTYMLQINPDSSINPDHLSYFR 456  
 Db 416 IPFSEGBGLDGGTAREWFLLSHEVNPMLCFEPAGKDNQCLQINPASYINPDHLSYFR 475  
 Qy 457 FVGRLMGLAVPHHYINGGFTVYKOLGKPIQLSDLESYDPELHKs-----PA 516  
 Db 476 FIGFIAFLFRRKFIDTGFSLFQYKRLNPKVGDLESDFPELHKsLWVKENNIEBC 535  
 Qy 517 -LDTHTPCVHNAGRILQHELKGPNRGPVTPTEENKEYVRLYVNWFMRGIEAQPLALQK 575  
 Db 536 DLNENYFSVDEKILGEIKSHDLRKGNGNVLTEENKEYIRMAEWRSLRSGEEOQAFFE 595  
 Qy 576 GNEFLIPQHLLKEFDQELELIGGLDIDANDWSNTRLHCVADSNTVRFNOAVETF 635  
 Db 596 GNEFLIPQYQLOFDACELEVILGQKQEDILNDWQHATYRHYARTSKQLMWVQFVKEI 655  
 Qy 636 DEEPRARLQFVQGSTRVPLQFKAQGSPFLTHLIDANTDNPKATTCFNR1 695  
 Db 656 DNBERMRLQFPTGTCLPVGSFADLGSN--GPQKFCIEKV-GKENWLPRTSHCFNRL 711  
 Qy 696 DIPPYESEKLYKLLTAVEETCGFAVE 723  
 Db 712 DLPPYKSFQLNKEKLLPAIETEGFQG 739

RESULT 11  
 US-10-097-534-10  
 Sequence 10, Application US/10097534  
 Publication No. US20030049607A1  
 GENERAL INFORMATION:  
 APPLICANT: GREENER, TSVIKA  
 APPLICANT: MOSKONTZ, HAIM  
 APPLICANT: REISS, YUVAL

APPLICANT: ALROY, IRIS  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL  
 MATURATION  
 CURRENT APPLICATION NUMBER: US/10/097,534  
 CURRENT FILING DATE: 2003-03-12  
 PRIOR APPLICATION NUMBER: 60/275,224  
 PRIOR FILING DATE: 2002-01-12  
 PRIOR APPLICATION NUMBER: 60/308,958  
 PRIOR FILING DATE: 2001-07-31  
 PRIOR APPLICATION NUMBER: 60/340,170  
 PRIOR FILING DATE: 2001-12-07  
 NUMBER OF SEQ ID NOS: 71  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 10  
 LENGTH: 739  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 +10-097-534-10

Query Match	Score	Length	Start	End	Mismatches	Gaps
Bee7 Local Similarity	32.1%	739;	32.1%	1245 5;	DB 15;	Length 739;
Matches 274	39.8%		39.8%	Fred. No. 7.3e-105;		
Conservative Matches	135;		99;	Mismatches 180;	Indels	Gaps
114 NPSDTDAVRGGIVVSL	---	---	114	QTRBDIG-TGGSVYDRCGLLENEGTYYEDSGPGRPLSFC		
109 SPSATSESDGGSTGSLPPNTNTSEGATGGLIPL	---	---	109	SPSATSESDGGSTGSLPPNTNTSEGATGGLIPL-----TISGSGP-RPLNPV		
168 MEEPAVTDGSTGAAGGGNCFVESSQDQLQAQLRNPPVRSGL	---	---	168	MEEPAVTDGSTGAAGGGNCFVESSQDQLQAQLRNPPVRSGL-----QTPQNQ		
160 TQAPLP-----	---	---	160	TQAPLP-----LGWEQY-----DQHGRYYVVDHEVKRTTWDR		
220 PHGHQSDELPEGYEQRITVQGQVFFLHTQTGVSTWDPRIP-----	---	---	220	PHGHQSDELPEGYEQRITVQGQVFFLHTQTGVSTWDPRIP-----		
193 PE-----PLPGWERRVTDNGMIRYYDDHFTRTTQWRPTLESVRYEQWQLQRSQGAM	---	---	193	PE-----PLPGWERRVTDNGMIRYYDDHFTRTTQWRPTLESVRYEQWQLQRSQGAM		
261 -----RDL-----NSYNCDELGPLPQGWVRSVTSRGRIFYDHDNRTQTFIDPRL	---	---	261	-----RDL-----NSYNCDELGPLPQGWVRSVTSRGRIFYDHDNRTQTFIDPRL		
248 QOFNQRPIYGNQNDLFTATSQSFKEPDPLGPPOWERKTDNSGRVFTHNNTITQNEQDPR-	---	---	248	QOFNQRPIYGNQNDLFTATSQSFKEPDPLGPPOWERKTDNSGRVFTHNNTITQNEQDPR-		
306 HTHMNHQCLKEPSQPLP-----	---	---	306	HTHMNHQCLKEPSQPLP-----PSEGSLDEELPAQR		
307 -----SQCQLINE-----KPIPEGMEMRFTYDGIYFVDHNRRTTYIDPTGKSALDNGPQIA	---	---	307	-----SQCQLINE-----KPIPEGMEMRFTYDGIYFVDHNRRTTYIDPTGKSALDNGPQIA		
340 YERDLQKLKVTR-----HELSLQQPAQHCRTEVSREBIEFESYRQIMKMRPKDJKKGRMLV	---	---	340	YERDLQKLKVTR-----HELSLQQPAQHCRTEVSREBIEFESYRQIMKMRPKDJKKGRMLV		
360 YTRDFKAVQYERFWMCQOLAMHQ-----HIKITVTRKTLFEDSFQQMSFSQDRLRRLAW	---	---	360	YTRDFKAVQYERFWMCQOLAMHQ-----HIKITVTRKTLFEDSFQQMSFSQDRLRRLAW		
397 KPRGEGLDYGVARENYLHLHEMINPYYGFLFOYSTNDNIMLOINPDSSINPDHLSYFH	---	---	397	KPRGEGLDYGVARENYLHLHEMINPYYGFLFOYSTNDNIMLOINPDSSINPDHLSYFH		
416 IIPGEGEGLDYGVARENYLHLHEMINPYYGFLFOYSTNDNIMLOINPDSSINPDHLSYFH	---	---	416	IIPGEGEGLDYGVARENYLHLHEMINPYYGFLFOYSTNDNIMLOINPDSSINPDHLSYFH		
457 FVGRGMLAVFHQYINGGTFPVKQLLGKPTQLSDLESVPELHSKLWVLENDITPV	---	---	457	FVGRGMLAVFHQYINGGTFPVKQLLGKPTQLSDLESVPELHSKLWVLENDITPV		
476 FIGRFIAMALFGKFDTGSKLSPYKRILNKVGGLDLESDEPEFTNSLWVYKNNIEEC	---	---	476	FIGRFIAMALFGKFDTGSKLSPYKRILNKVGGLDLESDEPEFTNSLWVYKNNIEEC		
517 -LDHTFCVHNNAFGRILOHLEKENGRNRPVTEENKCEYVRLVWNWFRMGRIGEAQFLAQK	---	---	517	-LDHTFCVHNNAFGRILOHLEKENGRNRPVTEENKCEYVRLVWNWFRMGRIGEAQFLAQK		
536 DLEMYSFSDKELEGEIKSHDLRPNGNLIVTEENKEEYIYRWAELRSRGBEQTQAFFE	---	---	536	DLEMYSFSDKELEGEIKSHDLRPNGNLIVTEENKEEYIYRWAELRSRGBEQTQAFFE		
576 GFNELIPOHLLKPFDOCKLELITIGGLDKIDLNWKSNTRLKHCVADSNIVRNWQAVETF	---	---	576	GFNELIPOHLLKPFDOCKLELITIGGLDKIDLNWKSNTRLKHCVADSNIVRNWQAVETF		
596 GFBILPQYQIFDAAKELVICGMQEDLNWKSNTRLKHCVADSNIVRNWQAVETF	---	---	596	GFBILPQYQIFDAAKELVICGMQEDLNWKSNTRLKHCVADSNIVRNWQAVETF		
636 DEERRARLQLQFYTGSTRVPLQGFKAQGSGAAGPRLFTIHLIDANTDNPLKAHTCENRI	---	---	636	DEERRARLQLQFYTGSTRVPLQGFKAQGSGAAGPRLFTIHLIDANTDNPLKAHTCENRI		
656 DNEKRMRLQLQFVTGTCRLPVGGPADLGSN-----GPQKFCIEKV-GKWNWLPRSHCFNRL	---	---	656	DNEKRMRLQLQFVTGTCRLPVGGPADLGSN-----GPQKFCIEKV-GKWNWLPRSHCFNRL		
696 DPPYESYBKLYSKLITAVEETGFAVE 723	---	---	696	DPPYESYBKLYSKLITAVEETGFAVE 723		
712 DLPPYKSYEQLKEKLLFAITEETGFGQE 739	---	---	712	DLPPYKSYEQLKEKLLFAITEETGFGQE 739		

725 DLPPYKSYEQLKEKLLPAIBETEGFGQE 752

QY 341 ERDIVOKUKLRLHELSLQQPQAGHCRIEVSREETPEESYRQIMK-I-RPKDLKGRMLVKFR 399  
 QY 453 SRETKQKDYFRKLKRPADENRFLRKHNNEESTRIMSTRPDKLARWIBTE 512  
 QY 400 GEBGLDYGVAREWYLICHEMLNPYGLFOYSTNIMYQINPSSI-NPDEHLSYFHFV 458  
 Db 513 SERGLDYGVAREWYLICHEMLNPYGLFOYSTNIMYQINPSSI-NPDEHLSYFHFV 572  
 QY 459 GRMNLAVEHGHIYNGCPTPYKQZLKGKIQSOLSESDPFLHSIWLNLNDITPVLID 518  
 Db 573 GRVQGLAYEVHKLDGFIRTPYKQMLGKQITLNQMSVDESEYNNLSKNTLNDTE-LD 631  
 QY 519 HTFVEBEAAGRILQHELKPGNPNVPTBENKEFVYLYTNWRFNNGIEQFLAQKGN 578  
 Db 632 IMFCIDENEENFGQTQVDLKPNSEIATVNENKREVIDLVQWRFNRYVOMNAFLEGFT 691  
 QY 579 ELLFQHLLKXPDXELELIIGGLKDLDNWKSNTPLKHCVADSN-IVRMFWQAVETFDE 637  
 Db 692 ELLFDLXKIFDENELLEMCGSLGDDVNDVRQHSTYKNGYCPNPIVQFWKAVLMDA 751  
 QY 638 ERRARLLOFVTGSTRVPLQGFKALOGSTGAAGPRLTFLHIDANTDNLPKAHTCNRIDI 697  
 Db 752 EKRRILLQFVTGTSRPANGFALLYGSN--GPQIPLTIEON-GSPKELPRAHTCNRIDL 807  
 QY 698 PPVRSYKLYEKULATAETTCGF 720  
 Db 808 PPYTFEDREKLMMENAQGF 830

RESULT 14  
 US-10-097-534-9  
 ; Sequence 9, Application US/10097534  
 ; Publication No. US20030049607A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GREENER, TSVIKA  
 ; APPLICANT: MOSKOWITZ, HAIM  
 ; APPLICANT: REISS, YUVAL  
 ; APPLICANT: ALROY, IRIS  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL  
 ; FILE REFERENCE: PLV-001-01  
 ; CURRENT APPLICATION NUMBER: US/10/097,534  
 ; CURRENT FILING DATE: 2002-03-12  
 ; PRIORITY APPLICATION NUMBER: 60/275,224  
 ; PRIORITY FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: 60/308,958  
 ; PRIORITY FILING DATE: 2001-07-31  
 ; PRIORITY APPLICATION NUMBER: 60/340,170  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 995  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-097-534-9

Query Match 31.6%; Score 1228.5; DB 15; Length 995;  
 best Local Similarity 40.4%; Pred. No. 4.3e-103; Mismatches 103; Indels 93; Gaps 19;  
 Matches 276; Conservative 103; Mismatches 211; Indels 93; Gaps 19;

QY 93 LSNASRL----KDTGYORLDCKLNPSD----TDAVRGQ----TDAVRGQ----IVVSLQDR 134  
 Db 347 LSEELSRRLQITPDNSEQFSSLIQLREPSSRLRSCVTDAVAEQLHPPSPVAYVHTPG 406

QY 93 LSNASRL----KDTGYORLDCKLNPSD----TDAVRGQ----TDAVRGQ----IVVSLQDR 134  
 Db 347 LSEELSRRLQITPDNSEQFSSLIQLREPSSRLRSCVTDAVAEQLHPPSPVAYVHTPG 406

QY 135 IGTGGSV-VDCRGLL---ENEGTYEDSGPGRPLSCFMEEPAPTYDSTGAAGGGN-- 186  
 246 LPSWEEKRDAKGRTYVHNRRTTWT---RPMQLAEDGA---SGSATMSNHL 295

QY 187 ----CRFVEPSDQDORLQAORLNPDYRGSL---QTPQNRPHGHOSPE---- 227  
 296 IEPQIRRERSLSPLPTVTLISAPLEGAKDSVERAKTJLSNPQSPSPNSPKHQKVTO 355

QY 228 -LPEGYDORTVQGVYFLHQTGSTMHDPRIP---RDLNNSVNCDELGPLPGMEV 280  
 Db 356 SFLLPPGWNRIAPNGRPFIDNTKTWEDRKLKEPVNRSKTSINPNDLGPBPWNE 415

QY 281 RSTVSGRIVPFDHNRTRQFTDRLHIMNHCQLMKEPSQDPLPLSEGSLEDELPARY 340  
 Db 416 RIHDGRTFYDHSKTTQWDEPQLON-----PAITG-----PAITG-----PAITG 452

QY 457 IEPQIRRERSLSPLPTVTLISAPLEGAKDSVERAKTJLSNPQSPSPNSPKHQKVTO 516

228 -LPEGYEORTTYQGQYFLHTOTGVSTWHDPRIP----RDNSVNCDELGPLPPGNEV 280  
 517 SFLPGWENRIAPGRPFIDINTKTITWEDRKLKPVHRSKTSNPNDLGPLPGWEE 576  
 281 RSTYSGRIVFUDANNRPTQFTDPRIHMTNHQCQLKEPSQPLPSEGSLDEBEPQRY 340  
 577 RIHDLGRTTIDHSKTCQWEDRLLN 613  
 341 ERDLVQKLRLRHLSLQPOAHCRCREVSEBIEPESSYRQIMRM-RPDOLKRLMVKER 399  
 614 SREFKQDYFRKLKPKADIPNPRFEMWLHRNNIPESSYRIMSVRDPVILKARLWIEFE 673  
 400 GEEGDGGYARETYLLCHEMINPYGLFOYSTDNYMLQINPDSI -NPDHISYFHFY 458  
 674 SERKDGYYARETYLLCHEMINPYGLFOYSTDNYMLQINPDSI-NPDHISYFHFY 733  
 459 GRINGLAVPHHYINGGFTVFKQLLGPQIOLSDLSVDPFLHKSLLWILENDITPVLID 518  
 734 GRVAGLAVFGKLDDPFRPFYKOMMLKQITINDMSVDSSEYNTSLKWLENDDPT-LD 792  
 519 HTPCVCBNAFGRILQHELKPGNGRNVPYBENKEYVLYNWRMREGIAOFALQGFN 578  
 793 LMFCIDEENGQTQVDLKPGNSBIMMVNENKEYVILVIVQRVNRQMMNALEGFT 852  
 579 ELIOPHLKPFDOKELELLIGDKIDINDWISNTRLKHCVADSN -IVRNFWOAETFDE 637  
 853 ELLPDIDIKFEDNELLMCGLGDDVNDWRSHTXNGYCPNHPVTONWKAVLMDA 912  
 638 ERRABLQFTGSPVPLQGXKLOGSTGAAGBRLFTHLIDANTDNLPKAHTCFNRIDI 697  
 913 EKRTRLQFTGSPVPLQGXKLOGSTGAAGBRLFTHLIDANTDNLPKAHTCFNRIDL 968  
 698 PPIYESKEVKEVLTTAAVEETCGF 720  
 969 PPIYEFEDREKLIMAVENAQGF 991

JLT 15 0-205-823-275  
 Application No. US10205823  
 ERLAW INFORMATION:  
 APPLICANT: Shliegel, Robert  
 APPLICANT: Monahan, John E.  
 APPLICANT: Endge, Wilson O.  
 APPLICANT: Garmanapu, Manjula  
 APPLICANT: Gorbatcheva, Bella  
 APPLICANT: Hoerlich, Sebastian  
 APPLICANT: Kamaikar, Shubhangi  
 APPLICANT: Wonssey, Angela M.  
 APPLICANT: Ghatti, Karen  
 APPLICANT: Zhao, Xumei  
 APPLICANT: Anderson, Dustin  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF PROSTATE CANCER  
 FILE REFERENCE: MRI-044  
 CURRENT APPLICATION NUMBER: US10/205,823  
 CURRENT FILING DATE: 2002-07-25  
 PRIOR APPLICATION NUMBER: 60/108563A1  
 PRIOR FILING DATE: 2001-07-25  
 PRIOR APPLICATION NUMBER: 60/314,356  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/335,020  
 PRIOR FILING DATE: 2001-09-25  
 PRIOR APPLICATION NUMBER: 60/341,746  
 PRIOR FILING DATE: 2001-12-12  
 PRIOR APPLICATION NUMBER: 60/362,158  
 PRIOR FILING DATE: 2002-03-05  
 NUMBER OF SEQ ID NOS: 455  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 EQ ID NO: 275  
 LENGTH: 995

; TYPE: PRT ; ORGANISM: Homo sapiens  
 US-10-205-823-275  
 Query Match 31.6%; Score 1228.5; DB 15; Length 995;  
 Best Local Similarity 40.4%; Pred. No. 4.3e-103; Mi matches 103; Indels 93; Gaps 19;  
 Matches 276; Conservative 103; Mi matches 211; Indels 93; Gaps 19;  
 Qy 93 LSNAISPL----KDTGYQLDICKINPSD----TDAVRGQ----TVVSLOTRDR 134  
 Db 347 LSEELSRRLQITPDNGEQFSSLQREPESRLRSCSYTDAVAQGHJPPPSVAYHHTPG 406  
 Qy 135 IGTGGSV-VDCRGLL --- ENGETYVEDSGPGRPLSCFMEEBAPYDSTGAAAGGGN-- 186  
 Db 407 LPSGWEEERKDAGKRTYYVNNRRTWT---RPMQLAEDA---SGSATNSNNHL 456  
 Qy 187 ---- -CRFVESPSPDQRQLQAQRILRNPDVRSI----QTPQNPMPGHQSPE --- 227  
 Db 457 TEPOQIRRPRSSSPVTASPLEGAKDSPVRAVTDLSNPQSPQSYNSPRQHKVTQ 516  
 Qy 228 --LPEGYEQRTVQGYYFHTQTQVSTWDPRIP --- RDINSVNCDELGPLPGWEV 280  
 Db 517 SLLPGWEMRATPNGRPFFIDHNTKTTWDPRLKFPYHMRSKTSLSNNDLGPUPGWE 576  
 Qy 281 RSTVSGRIFYDHNNTTQTDPRAHHTHNNHOCCOKEPSQPLPLPSEGSLDEBEPQRY 340  
 Db 577 RHLDGDTFYIDHNSKITQVEDPRIN-----PAITG-----PAVVPY 613  
 Qy 341 ERDLVOKLVLRHELSLQOQAGHCRIEVSREEFEESYRQIMMM-RPDHLKCRLYMVKFR 399  
 Db 614 SREFKQDYPRKKPKPADLPNREMKHRRNFFEYTRRNSVQRDPVILKARLWIEFE 673  
 Qy 400 GREGGLYGGVAREWLYLCHMELNDYYGLFOYSTDNYMLQINPDSI -NPDHLSYFHFY 458  
 Db 674 SSKGDLGGVAREWFLSLSEMENYYGFEYSATDNTNLQINPDSI-NEDLSYFFI 733  
 Qy 459 GRIMGLAVFGRHYINGGFTPYKOLGKPIQSLDLESYDPELHKSLWILENDITPVD 518  
 Db 734 GRVAGLAVFGKLDDPFPYKOMLGQITNDMESVDTSEYTNLSKWLENDDPT-LD 792  
 Qy 519 HFPCVNEINAFCRILQHBLKENGRTVTEENKEYVRLXNNPFRMGERIAQFLAQGFN 578  
 Db 793 LMFCIDEENFGTYQVDLKENGSELMVNTNEKRYIDLVQWFRVNRQKONNAFLERT 852  
 Qy 579 ELLPQHLLKPPQKELELITGLDIDLNWKSNTRLKECVADSN -IVRNFWOAETFDE 637  
 Db 853 ELLPDILIKIDBNELLEMCLGQDFFTRPFYKOMLGQITNDMESVDTSEYTNLSKWLENDDPT-LD 792  
 Qy 638 ERRARLQFTGSTRVPLQGFKALOGSTGAAGPRLFTIHLIDANTDNLPKAHTCFNRIDI 697  
 Db 913 EKKRILQFTGSTRVPMNGFAELGSN --GPQJLFTEQW-GSPEKLPRANTCFNRIDL 968  
 Qy 698 PPYESKEVKEVLTTAAVEETCGF 720  
 Db 969 PPYETFEDREKLIMAVENAQGF 991

Search completed: February 20, 2004, 15:37:43  
 Job time : 36.9477 secs

result No.	Query Score	Match Length	DB ID	Description
1	1492.5	38.4	T37545	ubiquitin-protein
2	1471	37.9	766	ubiquitin-protein
3	1437	37.0	815	probable ubiquitin
4	1377	35.5	809	ubiquitin-protein
5	1341	34.5	786	ubiquitin protein
6	1241.5	32.0	820	ubiquitin-protein
7	1227.5	31.6	887	ubiquitin ligase N
8	1056.5	31.6	708	NEDD4 ORF1 - mouse
9	1026.5	26.4	671	probable ubiquitin
10	854.5	22.0	3839	related to TONI pr
11	848	21.8	3227	probable ubiquitin
12	784	20.2	4056	protein F14J16.10
13	780.5	20.1	1126	ubiquitin-protein
14	769	19.8	3268	hypothetical prote
15	669	17.2	889	hypothetical prote
16	627.5	16.2	310	DNA binding protein
17	604.5	15.6	221	hypothetical prote
18	530.5	13.7	874	E6-associated prot
19	484	12.5	807	probable ubiquitin
20	481.5	12.4	892	probable membrane
21	471	12.1	1142	hypothetical prote
22	466	12.0	1083	polyubiquitin-like
23	451	11.6	873	probable ubiquitin
24	444	11.6	1029	hypothetical prote
25	444	11.6	1054	hypothetical prote
26	444	11.4	1066	probable ubiquitin
27	418	10.8	1001	probable ubiquitin
28	400.5	10.3	655	HERC2 protein - mo
29	382.5	9.8	4836	probable ubiquitin

tail number of hits satisfying chosen parameters:	283308	arched:	283308 seqs, 96168682 residues	ALIGMENTS
minimum DB seq length:	0			RESULT 1
maximum DB seq length:	200000000			T37545
st-processing:	Maximum Match 100%			ubiquitin-protein ligase (EC 6.3.2.19) pub1 [validated] - fission yeast (Schizosaccharomyces pombe)
Database :	US-10-009-945-2			N; Alternative names: ubiquitin ligase Pub1
querence:	1 GSSSIKIRITVCAKNLAKK.....EKLYEKULLTAVETCGFAVE 723			C; Species: Schizosaccharomyces pombe
oring table:	BLOSUM62			C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Jun-2002
arched:	Gapop 10.0 , Gapext 0.5			C; Accession: T37545; T48655
				R; McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
				R; Salek, R.; Jia, Z.; Karamanis, J.; Young, P.G.
				Submitted to the EMBL Data Library, September 1997
				A; Reference number: Z21722
				A; Accession: T37545
				A; Status: preliminary; translated from GB/EMBL/DDBJ
				A; Molecule type: DNA
				A; Residues: 1-767 <MCL>
				A; Cross-references: EMBL:Z99161; PIDN:CA016207.1; GSPDB:GN00066; SPDB:SPAC11G7.02
				A; Experimental source: strain 972h-, cosmid C11G7
				A; Genbank ID: K020558
				A; Title: tolerance of low pH in Schizosaccharomyces pombe requires a functioning pub1
				A; Reference number: 207985; PMID:91940937; PMID:9197411
				A; Status: preliminary; translated from GB/EMBL/DDBJ
				A; Molecule type: DNA
				A; Residues: 1-767 <SAL>
				A; Cross-references: EMBL:U62795; NID:922262192; PIDN:AAB63350.1; PID:G2262193
				A; Experimental source: strain J227
				C; Genbank ID: U62795
				A; Map position: 1
				A; Intonations: 6/2, 14/1, 62/2
				C; Function: <UBI>
				A; Description: EC 6.3.2.19 [validated, MUID:96205868]
				C; Function: <CYC>
				A; Description: involved in of the mitotic activating tyrosine phosphatase cdc25 [valid
				C; Function: <TO1>
				A; Description: required for low pH-tolerance [validated, MUID:97340937]
				C; Superfamily: Yeast ubiquitin-protein ligase; WW repeat homology
				C; Keywords: cell cycle control; ligase
				P; 205-242-/Domain: WW repeat homology <WW1>
				P; 288-325-/Domain: WW repeat homology <WW2>
				P; 345-382-/Domain: WW repeat homology <WW3>
				Query Match Similarity 38.4%; Score 1492.5; DB 2; Length 767;
				Best Local Similarity 41.1%; Pred. No. 1. /e-100; Mismatches 118; Gaps 19;
				Matches 329; Conservative 118; Mismatches 234;
Qy				4 SIRRTIVLCAMLAKKDFPFLDPFPKTVUDGSGQCHSTDTVKTLDPKNNQHYLVG 63
Db				7 SRRRTIVVAAAGLYKRDVRFPEDFAVLTVDGE-QTTTTATKKTLPYNTTFEVNT 65
Qy				64 KTDSTISITSVWNAHKKTHRKQGAGFLCVRLLSNRSLKDGTGYBL-DLICKLNPSDIDAY 121

66 DNSIAIQYEDQKXF-KKRGQFLGVINLRYDVLDAIGGDEMTRIKKSN-ENTVV 122  
 122 RGQIIVSLO------TRDRIGGSVYDGRULNEGGDEMTRIKKSN-ENTVV 122  
 123 HGLIINSLTAQSTLQVSSAASGARTORTSNTDQSSSSYTSRNPASSRAGSPTRD 182  
 158 SGPG----REPLCFMEE---PAPY--TDSIG-AAA 182  
 183 NAPASASSEPRTESSFDQYRLLPPOWERITDNGRTYYVDHNTSTRSNTWIRNLSSVA 242  
 183 GGNCRCREVSPS----ODORLQQRNLNPDRGSLQTQNPRPHQHSPELPEGEQ 234  
 243 GAAABELHASSASSANVTEQVQEPSSNARTEASVLTNSATTAG----SGELPPGNEQ 296  
 235 RTTVOGQYVPLHTQTCSTWHDRIPDDNSY-DELOLPDMWEFWRST 283  
 297 RYTPGRGPFDVNDNTTRTTWDRDQQYIRSTGGPNNTATCQOPPSQOLPLPSWEXRLT 356  
 284 VSGRYYFDVNDNRTQFDPRLMHMHQCLKEPSQOPLPSESSLEDEBPAQRVERD 343  
 357 NTARVYFDVNDNTKTTWDPR----LPS-SL-DQNPV-QKRD 392  
 344 LVQKVKVLRHLSQQPAGKPCIEVSREEFEESTRQIMKRPDLKGRMLYKFRGSEG 403  
 393 FRRKLIVFSQPAL-HPLPGOCHIKVRNHLFEDSYAETNRQSATDLKGRMLKDGSGD 451  
 404 LDYGVAREVNLYLCHEMNPYGLFQXSTONIYMLQINPDSSTPDHLSYFHVGRLMG 463  
 452 LDYGLSLREYFFLISHEWFNPFCFLQYSSVNTYDQINPHSGINPEHLYFREFGRVIG 511  
 464 LAVFGHYYNGGFTVPFYKQLLGPIQSDLESVDELKHSVLWILNDITPVLDHTFCV 523  
 512 LAIHPHRFVDAFVTSFKYMLQKVTQDME5DAEYRSLVWILNDITGVLDLIFSV 571  
 524 EHNAAGRILQHLEKPGNGRNVPTEENKEYVRLYNNWRFNKGTEQFLALQKSFNELLIPQ 583  
 572 EDNCGEVFTIDLKPGNGRNIEETENKEVYDVLVTRIKRQEENAFHEGSEELLIPQ 631  
 584 HLKPFQDQEKELELITGGDIDKIDLNWKSNTRLKHCVADSNITVRNWOAVETDEERRARL 643  
 632 ELINVYDDEELLIGGSEIDMWDKKHDYSSKSENDOLIKFWELDNEWNECKSR 691  
 644 LQFTGSTRVPLQFCFKALQGSTGAAGRPLFTHLIDANTDNPKHCTCNRIDIPYYESY 703  
 692 LQFTGTGSTRVPLQFCFKDQGSD--GPRKFTTEA-GEPNKLPKHCTCNRLDLPYTSK 747  
 704 EKUVEKLITTAVEETCGFAVE 723  
 748 KDLDDHKLSTAAVEETIGFQOE 767

35652 ubiquitin-protein ligase (EC 6.3.2.19) - fission yeast (Schizosaccharomyces pombe)  
 ;Alternate names: E6-AP-like protein ubiquitin ligase  
 ;Species: Schizosaccharomyces pombe  
 ;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
 ;Accession: S66562; T45159  
 ;Name: Beach, D.  
 ;MBO J., 15, 1301-1312, 1996  
 ;Title: Pub1 acts as an E6-AP-like protein ubiquitin ligase in the degradation of cdc25  
 ;Reference number: S66562; MUID:96205868; PMID:8635463  
 ;Accession: S66562  
 ;Status: preliminary; nucleic acid sequence not shown  
 ;Molecule type: mRNA  
 ;Residues: 1-766 <NEF>  
 ;Cross-references: GB:U66716; NID:91519443; PID:91519444  
 ;Neisky, B.-S.; Beach, D.  
 ;Submitted to the EMBL Data Library, August 1996  
 ;Description: Pub1 acts as an E6-AP-like protein ubiquitin ligase in the degradation of  
 ;Accession: T45159  
 ;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA  
 A;Residues: 1-766 <NEF>  
 A;Cross-references: EMBL:Y07592; PIDN:CBA68867.1  
 C;Genes:  
 C;Superfamily: Yeast ubiquitin-protein ligase  
 C;Keywords: ligase  
 F;205-242;Domain: WW repeat homology <WW1>  
 F;288-325;Domain: WW repeat homology <WW2>  
 F;345-382;Domain: WW repeat homology <WW3>  
 Query Match 3.79%; Score 1471; DB 1; Length 766;  
 Best Local Similarity 40.9%; Pred. No. 6..3e-99;  
 Matches 327; Conservative 118; Mismatches 235; Indels 120; Gaps 20;  
 Qy 4 SIKRILTVCAKNLAKEDFERRLPDPFAKTVDFGGGCHSSTDYTRNTLDPKWNQHYDLYVG 63  
 Db 7 SRRRTVIVAADGLYKRDVERFDPFPAVLTVDGE QTHTTTAKTKLNPWNNETPEVNT 65  
 Qy 64 KTDPSITISVNHKRHKQAGAEFLGCVRLLSNAISRLKDTGYCQL--DLCKLNPSPDTDAV 121  
 Db 66 DNSTIALQYEDOKKF-KKKGGOFGLGVINLRGVDTDLAIGDEMILTRDKSN-ENTVV 122  
 Qy 122 RGQIIVSLO-----TRDRIGTGGSVYDRCGLLENEGTYED 157  
 Db 123 HKIIINLSTITAQSTLQVPSAAASGARTQRTSNTDQPSSKSSSVRNPASSRAGSPTRD 182  
 Qy 158 SGPG----RPLSCFMRM-PAPY--PAPY--TSTG-----AAA 162  
 Db 183 NAPASASSEPRTFSSFEDYGRGLPGWERTNLTGRTYVTDHNTNSTTWIRPNSSVA 242  
 Qy 183 GGNCNCRFYESPS-----ODQRLOAQERLNPDVYGSQTPONRPHGOSPELPEGEQ 234  
 Db 243 GAAADEHSSASSANTVEGVPSSPAARTEAVLTSNATAG----SGLPPPEWQ 296  
 Qy 235 RTTVOGQYVFLHTOTGVSTMHDPRIDLNSVN-----CDELGPLPPGWEVRLST 283  
 Db 297 RYTFGRGPYFVDHNTTWTDDPR-----LPS-SL-DQNPV-QYRVD 392  
 Qy 284 VSGRIFTYDHNNTTQFTDPRLHHMMHQCLKEPSQBLPLPSGSLLEDEBPARYRD 343  
 Db 357 NTARYFVDHNTTWTDDPR-----LPS-SL-DQNPV-QYRVD 392  
 Qy 344 LQVQLKVLRHLSLQOPQAGHCRIEVSEEFESYQIMKRPDKLKRLMYKFRGSEG 403  
 Db 393 FRKLIXYLSQPL-HPLPGOCHIKVRNHFESYAEIMRQSATDJKRKMTKDFBDG 451  
 Qy 404 LDYGVAREVNLYLCHEMNPYGLFQXSTONIYMLQINPDSSTPDHLSYFHVGRLMG 463  
 Db 452 LDYGLSLREYFFLISHEWFNPFCFLQYSSVNTYDQINPHSGINPEHLYFREFGRVIG 511  
 Qy 512 LAIHPHRFVDAFVTSFKYMLQKVTQDME5DAEYRSLVWILNDITGVLDLIFSV 571  
 Qy 524 ERNAGFGRILQHLEKPGNGRNVPTEENKEYVRLYNNWRFNKGTEQFLALQKSFNELLIPQ 583  
 Db 572 EDNCGEVFTIDLKPGNGRNIEETENKEVYDVLVTRIKRQEENAFHEGSEELLIPQ 631  
 Qy 644 LAWFGHYYNGGFTYPYKQLGKPIQLSPLSVDPLBEKSLWVILENDITPVLDATFCV 523  
 Db 691 LQFTGSTRVPLQFCFKALQGSTGAAGRPLFTHLIDANTDNPKHCTCNRIDIPYYESY 703  
 Qy 704 EKUVEKLITTAVEETCGFAVE 723  
 Db 747 KDLDDHKLSTAAVEETIGFQOE 767

## RESULT 2

35652 ubiquitin-protein ligase (EC 6.3.2.19) - fission yeast (Schizosaccharomyces pombe)  
 ;Alternate names: E6-AP-like protein ubiquitin ligase  
 ;Species: Schizosaccharomyces pombe  
 ;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
 ;Accession: S66562; T45159  
 ;Name: Beach, D.  
 ;MBO J., 15, 1301-1312, 1996  
 ;Title: Pub1 acts as an E6-AP-like protein ubiquitin ligase in the degradation of cdc25  
 ;Reference number: S66562; MUID:96205868; PMID:8635463  
 ;Accession: S66562  
 ;Status: preliminary; nucleic acid sequence not shown  
 ;Molecule type: mRNA  
 ;Residues: 1-766 <NEF>  
 ;Cross-references: GB:U66716; NID:91519443; PID:91519444  
 ;Neisky, B.-S.; Beach, D.  
 ;Submitted to the EMBL Data Library, August 1996  
 ;Description: Pub1 acts as an E6-AP-like protein ubiquitin ligase in the degradation of  
 ;Accession: T45159  
 ;Status: preliminary; translated from GB/EMBL/DDBJ

9744	ubiquitin-protein ligase [Imported] - Neurospora crassa	Db	642 TNENKEKYVELMKVRIERIEKTEQQPRAFDGEHLLIPOLINVEDEREELLLGGIAEID 701
Alternates:	Protein B24B19_160	Qy	606 INPKWSNTRLKHCVADSNTIVRFWQAVETDEEARLQLQFVTGSTRVPLQGKALQST 665
Species:	Neurospora crassa	Db	702 VDDWKHTDHYGYTESDEVIOFFQWTVRSDGEQKSRLIQTFTTSRLEPVNGPDLQSSD 761
Date:	02-Jun-2000 #sequences_revision 02-Jun-2000 #text_change 18-Aug-2000	Accession:	666 GAPGRPLFTIHLDANTDNLPAKHTCFNRIDIPPESYEKLVEYLTAVEETCCFAVE 723
Schulte, U.; Aigr, V.; Rohselsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000	Qy	762 --GPRFTIEKAGEIT-NLPKAHTCFCNRDLPPYKSLMQLQQTIAVEETMGFGQE 815	
Reference number:	Z25022	Db	
Accession:	F49744		
Status:	Preliminary		
Molecule type:	DNA		
Residues:	1-115 <SCH>		
Cross-references:	EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19_160		
Experimental source:	BAC clone B24B19; strain OR7A		
Genetics:	NCSP:B24B19_160		
Gene:	NCSP:B24B19_160		
MAP Position:	6		
Introns:	11/1; 24/1; 59/2; 110/1; 783/2		
Supersource:	Yeast ubiquitin-Protein ligase; WW repeat homology		
239-276/Domain:	WW repeat homology <WWR1>		
334-371/Domain:	WW repeat homology <WWR2>		
393-430/Domain:	WW repeat homology <WWR3>		
Query Match	37 0% Score: 1437 DB: 2; Length: 815;		
Best Local Similarity	38.3%; Pred. No. 2, 1e-96;		
Matches	321; Conservative: 125; Mi.matches: 238; Indels: 154; Gaps: 21;		
9	ITVJACKNLAKKDFSLPLDPFAKIVWDGSGQGCNSDTVYKNTLDPKMNHOHDLY-----V 62		
9	LPVIAADGLYGRDVRFPDFPAVINGE-QTKTIVQVSRTINTPYNNHEFDWLQISQSKV 67		
63	GKTDISITSYNNHKTHKKQAGAGTGCVRL-LSNAILSLRKDIGYQRLDLCKLNPSDTDAY 121		
68	NEDSLLAVQVQDQKTP-KKCDQGFGLGVINRQVYIELAPDAQMLTRDLEKSTNLVV 126		
122	RQIQIVSLSQTR----DRIGTGGSVVDRCOLLENEGTVYED----SGP----- 160		
127	HGKLINLNLSTLTATMSRLGPPSSSSRPSLTPQSVSINDRANERPSSAVSGPNTGATT 186		
161	----GRPLSCFMEE-----PA-----PYTDSTS----- 179		
187	MTLARSPASLAVSSSSTAPTFGTNGTAPINPSTLVQAQRHHSTLSPEDSMGRLLPAGWE 246		
180	----AAAGGCNCNCRFVEPSQDORLQAQLRNPDVRSQSLQ 215		
)	247 REEDHLRERTYVDHNSRTTSINRPPTGTALENTRABANQVERORHQNRTLPDRTGANS 306		
)	216 PQNRP-----GHQSP---ELPEGYQRTTIVOGQVYFLHTOTGSTMWHDR 258		
)	307 PTIQQQQAATAANATMMHTGATTGTTGELPAGWQRFPEGRGFFYDVHNTTRTWYDPR 366		
)	259 IPDL-----NSVN-----CDELGPPLPGWERTSSTVSGRYFVDENRNTTOFDPRL 305		
)	367 RQYIRAYGGQNTGTTQCPVSQLGPGLPSGWNRLLNTARYFVDNTKTWTWDRP 425		
)	306 HHIMNHQHQLKEPSQPLPLPSEGSLDEELPAQYERDLYQKLVRLHELSLQOPQAGHC 365		
)	426 -----LPS-----SL-DQNP-----QYKRDPERKLIVYERSPAM-RIMSGQC 461		
)	366 RIBVSREBIEEFSYRQIMKRPKDLCRKLNVKFSESEGLDYGGVAREWYLLCHEMLNPY 425		
)	462 HIKYTRSHIFEDSFAEISRSQSATDLCKRLMIKFDGEDGLDGGILSREFPFLSHEMFNP 521		
)	426 YGIFQYSIDNTYMLQINPDILSYRPPVGRVLRMGAIAVFGHRYINGGFTFYKOLL 485		
)	522 YCLFEYSAHDNTYTLQINPHSGINPEHANYFKFIGRVGLAIFHRFLDFFIGLYKANVL 581		
)	486 GKPLQLSDLESYDPELKHSLYWILENDITPYLDHFTCFVNEAFCRGLQHBLKPNGRNPYV 545		
)	582 GRASLADMEGVDAFERSLQNLNDITDITDFTSEDERFGVITEDLINGRNIAV 641		
)	546 TERNKKEYVRLYNNWRMRGIBAQFLALQKGFNELIPOHLLKPFQKELELIGGLDKID 605		
	RESULT 4		
	S4317 ubiquitin-protein ligase (EC 6.3.2.19) RSP5 - Yeast (Saccharomyces cerevisiae)		
	N; Alternate names: EGAP-like protein ubiquitin ligase; protein YER125w; PUB1 protein		
	C; Species: Saccharomyces cerevisiae		
	C; Date: 10-Sep-1999 #Sequence revision 10-Sep-1999 #text_change 03-Jun-2002		
	C; Accession: S43217; S50628; S70050		
	R; Mulligan, J.T.; Dierrich, P.S.; Hennessy, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor submitted to the EMBL Data Library, February 1993		
	A; Reference number: S30812		
	A; Accession: S43217		
	A; Molecule type: DNA		
	A; Residues: 1-809 <MTL>		
	A; Cross-references: GB:U18916; EMBL:U18916; PIDN:91384128; PIDN: AAC03223.1; PID: g603364		
	R; Dietrich, F.S.		
	A; Description: The sequence of <i>S. cerevisiae</i> cosmids 9781, 8198, 9115, 9981, and Lambd		
	A; Reference number: S50628		
	A; Molecule type: DNA		
	A; Residues: 1-809 <Die>		
	A; Cross-references: ENB:U8916; PIDN:91384128; PIDN: AAC03223.1; PID: g603364; GSPDB:GN0		
	R; Hein, C.; Sprinzel, J.Y.; Volland, C.; Hagnauer-Tsapis, R.; Andre, B.		
	Mol; Microbiol, 18, 77-87, 1995		
	A; Title: NPII, an essential yeast gene involved in induced degradation of Gap1 and Fur		
	A; Reference number: S70050; MUID: 96154942; PMID: 8596462		
	A; Accession: S70050		
	A; Status: nucleic acid sequence not shown; not compared with conceptual translation		
	A; Molecule type: DNA		
	A; Residues: 1-101 <HEI>		
	C; Function:		
	C; Superfamily: Yeast ubiquitin-protein ligase		
	A; Gene: SGD:RSP5; PUB1; NP11; MIPS:YER125w		
	C; Key words: ligase		
	A; Cross-references: MIPS:YER125w; SGD:S0000927		
	A; Map position: 5R		
	C; Function:		
	C; Description: involved in endocytosis of GAP1 protein and FUR4 protein; binds and ub1		
	C; Superfamily: Yeast ubiquitin-protein ligase		
	F; 229-266/Domain: WW repeat homology <WW1>		
	F; 3331-368/Domain: WW repeat homology <WW2>		
	F; 387-424/Domain: WW repeat homology <WW3>		
	Query Match	35.5% Score: 1377; DB: 1; Length: 809;	
	Best Local Similarity	37.0% Prod. No. 4.8e-22; Prod. No. 4.8e-22;	
	Mismatches	131; Indels 164; Gaps 24;	
	Matches	313; Conservative 131; Mismatches 238; Indels 164; Gaps 24;	
	3 SSIKRLRTVLCNLAKEDFRRPDPFKTIVVGDGCHSTPVTQNLDPQRNQHDL-Y 61		
	3 SSISYKL--VAEELYKRDVPRPDPFAVLTDIGY-QTKTSISAAKTTLNPWNTEFKDD 59		
	62 VKUDSITISVMMNEKKTHKKQAGAGTGCFLGCCVRL-LSNASRLKD-----TGYOR----LDL 110		
	60 INENSLTQVFDKRFK-KRQDGFLGLVNVYGVDFLGHMLDDEDTASSGRREETITRDL 118		
	111 CKLNPSDSTDAAVRGQIVV-----SLOTDRIGTGGSVVDGRGJL 148		
	119 KRSN--DGMASVGLIVVLSKLSSSPHSQAPSHTASSSTNTSSTRNCHSHTSS--T 173		
	149 ENGETVYEDSGPRLSCMEEBAP-----YTDSTGAA-		
	174 RNHS7SHPSRGTAQAVESTLQSQSTTAATNTATSHRSTNSTSSATROYSSPFDQYGRLLPP 233		

183 -----GGGNCREVE-----SPSQDQLQAOQLRNPDVRSQQLQTQFQRN-----PHG 222  
 234 GWERRTDNFGRTYDDHNTTRTTWKRPTLDQ-TEARGNOLNANTELERQHRGRTLPGG 292  
 223 HQS -----PELPGNEQRITVQGOVYFLT 247  
 293 SSNDNSVTQVGGSNNIPPVNGAAAFAATGGTSGLGEPSGNORFPEGRAYFVDH 352  
 248 QTGYSTWHDERPIPDLSN-----CDBELGPUPPGMEVRSTVSGRYFVDHNRN\* 297  
 353 NTRITTWDERQQRQVITYGPTNTTICQOPVSOLGPSPGHMRLINTARYFVDHNTKT 412  
 298 TOFTDPRHLHMNHCOLKEPSQPLPSEGSLDEEPAQYERDVLQKLVLHELSL 357  
 413 TWDDPR-----LPS-SI-DQNP-----QYKFRFRKTYFSSQPAL 448  
 358 QQPQAGHCRLEVSREIEEEFSYRQIMKMRPKDILKRLMKVKGFECEHDYGGVAREWLWLL 417  
 449 -RILPQOCHIKVRRRNIFEDAYQEMIRQTPEDLKRMLMIKEDGEEDGYGVSRFFLL 507  
 418 CHEMNPNPYGLFOYSTDNNTYMLQNPDSINPDHLSYTFEVGRIMGLAEVIGHYINGGET 477  
 508 SHMMPNPFCYLFEVSDAYDNNTIONPNSGNCINPBLNTYKPIGRVGVGFRRFLAFFV 567  
 478 VPFYKQULGPQLQSDLESVDPLEHKSLSWILENDITPVLDHTFCVHENAFGRLOHELK 537  
 568 GALYKOMMLRKCKVLDQMEGYDAEVYNSLNMTLNSIDGVLTFSADDERFGEWVVDLK 627  
 538 PNRGAVPTEENKKEYVRLYVNWTRMRGTEAQFLAQKGFNEILIPQHLLKPPDQELELI 597  
 628 PDGRNIEVTGDKKKEYVELYTQWRIVDRQEOQFAFMGGENELIPEDLYTVEDESEELL 687  
 598 IGGIDKIDLNWKNSTRKLHKCVADNTIVWFWQAVETFEBERARLQOFUTSTRVPLQG 657  
 688 IGGIAEDIEDWKRDHYDGYQESSEBIVQFWKCVSEWDNEQARLQOFUTGTSRIPNG 747  
 658 FKALCGSTGAAGPRLFTIHLIDANTDNLPAKHTCFNRDIPPYESVERLYEKULLTATEET 717  
 748 FDLDQGSD-----GPRRFTEKA-GTVQQLPKRSHTCFNRVUDLPQYDMSMKQRLTLAET 803  
 718 CGFAVE 723  
 804 IGFQGE 809

ISU75  
 19585 ubiquitin protein ligase - fission yeast (Schizosaccharomyces pombe)  
 ;Species: Schizosaccharomyces pombe  
 ;Date: 03-Dec-1995 #sequence\_revision 03-Dec-1999 #text\_change 18-Aug-2000  
 ;Genetics:  
 ;Gene: SPDB:SPBC16E9.11c  
 ;Map position: 2  
 ;Intron: 60/2  
 ;Superfamily: yeast ubiquitin-protein ligase; WW repeat homology <WW1>  
 ;Submitted to the EMBL Data Library, August 1997  
 ;Reference number: Z21865  
 ;Accession: T39515  
 ;Status: preliminary; translated from GB/EMBL/DDBJ  
 ;Molecule type: DNA  
 ;Residues: 1-786 <VOL>  
 ;Cross references: EMBL:299759; PIDN:CA16903.1; GSPDB:GN00067; SPDB:SPBC16E9.11c  
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 ;Genetics:  
 ;Gene: SPDB:SPBC16E9.11c  
 ;Map position: 2  
 ;Intron: 60/2  
 ;Superfamily: yeast ubiquitin-protein ligase; WW repeat homology <WW1>  
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 ;306-313/Domain: WW repeat homology <WW3>  
 ;364-401/Domain: WW repeat homology  
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Qy 6 KIRLTVLCAKNAKKDFFERLDPDPAKIVVUDGSCQCHSTDVKTIDPKWNQHLYDLYVGKT 65  
 Db 7 RYRFYIVAAQDLGSKDLFQDPAILVDE-QTHTKVIKSVNPNVYNEGFEVTVKPS 65  
 66 DSITISWANHHKKHKKOGAGFLGCYVLLSNASLRKDGTQYR---LDLCK-LNPSTD-  
 66 SVISIRLFQKFK-KRKDQFLGIVSF----RMREVGFSRSNREVSLTRPKSSSTN 118  
 120 -AVRGQIVV-----SL 129  
 119 LSVLGNLVLKVAPSKIRAPAGNHSSSTANRTTSTPTTTARTTRTPPTATNTSNSQST 178  
 130 QPRDRIGTGGSVVDCGELLENGETYEDSGPGRDL-----SCFMEEPA----PYTDS 177  
 179 SNTSTRGTSAAATNSGNTGAGTGASHRSS---PVTNRQTNNTSALSNSNAHMSFSDQ 234  
 178 TGAAGG-----GNCRTEV-----SPSODRBLQARLRLRNPDV 209  
 235 YGRLPPGMERRADSLGRTYYTDHNTRTTWTTRPASSTNPVHNNTSDDSQELNHQRHLPD-  
 210 RGSLCTQNPRPFGHQSP--'BLPEGEYQRTVQGGYFYLTQGTTGAGTGTGAGT 260  
 294 -----DSNPBLMQSDGSNDLPGWMEMRTDTGPYFVDHNTTTWDPNPLFLVRENG 346  
 261 -----RDLSNSYNCDELGPGLPGWEVRSTVSGRYFVDUNNRTTQFTDERRHHIMNHOCQ 314  
 347 GSTVGSMQPSLQPSLHGLPLPGWERNLTTNSARVTFVDNTKTTWDQRL-----397  
 315 LKEPSPQPLPSEGSLDEEPAPQYERDLVQKLXRLHLSLQOFOAGHCRITVSREETI 374  
 398 -----PSALDQDV-----QVKCDPFRKLFLYFRSOPGM-RPLPGOCNVYVRRDHII 441  
 375 FEDSYRQIMKARFDLKKBLMKYKPGEGEGLDGYVARENTYLKCHEMINPPYGLFOYSTD 434  
 442 FEDSYAELMRYSAHD;KCRKLMTFREDGSDGLYGGISREFFFLSFRKMFDPYCFEYSAV 501.  
 435 NTMLQINPDSSENPDHLSYFFFGRIMGLAVFHGHYINGGFTVBFYKQOLLKPIQLSDL 494  
 502 DNTLQINPFSNSNPHEUNYPFGRVLAEDHFGVTRVTLITNGENTEVENKKKCYV 561.  
 555 RLYTNWRPMRGIBAOFLAOKGFLNELLIPQHLLKPFQKELIELIGSLDKDNLNQKSNTR 614  
 495 ESDPELLKSLVWILENDITPVLDHFCVNEAAGRLQHLPKNGRNVTENKKEYV 554  
 Db 622 DLVTEWRSKRVBQQFNAYSGTVELVLSPLVNVDEREELIGGSDYDVEDWKSHTE 681  
 615 LKHCVADSNIVRNWQAVETDEERRRLQFVTGSTRVPLQFKALGSTGAAGPRLFT 674  
 682 YRTVIAEDPVKNTWELLAGKNEDRKLQFQATGTSRIPGFRLQLQSD---GPKFET 738  
 675 IHLDANT-DNLPAKHTCFNRDIPPYESYKLYEKULLTATEETCGFAVE 723  
 739 IE-KAGTPDQPLPVANTCENRLDIPYSKDTTHEKLSLAVENTVFGNE 786  
 Status: Preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-120 >AAA>  
 A; Cross-references: EMBL:AL137469



615	NEHDHSYFKEIGRVAAGMAYHGKLLDGFFIRPFYKQMLQKLITLHDMESVDEYYSSLRW	674	QY	423	NPYXGLFOYSTNDNITYMLQINPDSST-NPDPHLSTYHVGRIIMGLAVFHGHYTNGGFTVYPFY	481	
508	IENLITPVLDHTCVERNAEGRFLQHBLKPGRNVPTEENKKEVRLVNWRMRGIE	567	Db	380	NPYGYREYSATDNTLQINPNSGCNEQHLSFKFGRVAGHAVHKKULLDFIFRPFY	439	
675	ILENPTE-LDLRFITIDEELFGQTHQELKTGGSEUVTNKKECTYLVONREVNRQ	733	QY	482	KQLIGKPIOLSDLESYDPELHKSLWILENDITPVLDHTFCVHNAAFRGILQHELKNGR	541	
568	AQFLALOKGENELPQHLLPKPFDKELELLIGGLDKIDLNWDKSNTFLKCHCVA-DSNIYR	626	Db	440	KMLQLKLTHMDMSYDSEYYSSRWRILENDPTSLDIFLFDIPELFGOTHEELKTGGS	498	
734	RQNAFLAKFEGFELLPQDLIKIDNENELEMCGLGDDVNDREHRYKNQYSLNHQVH	793	QY	542	NVPVTBENKEYVRLXVNMRMGRIBEAQFALQGENELPQHLLPKPFDKELELTIQGL	601	
627	WENQAVETPDERRARLLOFVTGSTRVPLQFKAQSSTGAAGPRLFTIHULIDANTDNL	686	Db	499	ERVVTNNKNCVKYVLYTQWQFVNTRQKONAFAFKEFELIPQDQIKIDNEELLMGGL	558	
794	WFWKAVLNMDSERKTRLLQFVTGSTRVPLQFKAQSSTGAAGPRLFTIHULIDANTDNL	849	QY	602	DKIDLNWDKSNTFLKCHCVA-DSNIYRWFNOAVEFDEERARLQFVTGSTRVPLQGPKA	660	
687	KAHTCPRNIDIPPVASYKELYKLTAVETCF	720	Db	559	GVDVNDWREHTKYKNGSYNSNHHQVTHWFKAIVMWMDSERIRLQFVTGSTRVPMNGFAE	618	
850	RAHTCENRDLDPYPSFDELWDKLQMAIENTQGF	883	QY	661	LQGSTGAGAPRLFTI	675	
			Db	619	LNGSN--GPQSFIV	630	
<b>SJLT 8</b>							
3196	DD-4 ORF - mouse (fragment)			RESULT 9			
	Species: Mus musculus (house mouse)			T37900	probable ubiquitin-protein ligase - fission yeast (Schizosaccharomyces pombe)		
	Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000			C;Species: Schizosaccharomyces pombe			
	Accession: 183196			C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Aug-2000			
	Kumar, S.; Tomooka, Y.; Noda, M.			R.Bieger, M.; Mc Dougall, R.C.; Rajandream, M.A.; Barrell, B.G.			
	ochem, Biophys. Res. Commun. 185, 1155-1161, 1992			submitted to the EMBL Data Library, September 1999			
	Title: Identification of a set of genes with developmentally down-regulated expression			A;Reference number: 221752			
	Reference number: 160-67; MUID:92328780; PMID:1378265			A;Accession: T37900			
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	Residues: 1-708 <R>			A;Cross-references: EMBL:AU117390; PIDN: CAB55856-1; GSPDB: GN00066; SPDB: SPAC1805.15C			
	Cross-references: GB:DI0714; NID:9220508; PID:9220509			A;Experimental source: strain 972h; cosmid c1805			
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	Gene: NEBD-4			C;Genes:			
	Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiquitin repeat homology <WW>			A;Map position: 1			
	196-233/Domain: WW repeat homology <WW2>			A;Introns: 60/2; 105/1; 639/2			
	251-38/Domain: WW repeat homology <WW3>			C;Superfamily: WW repeat homology <WW>			
	347-682/Domain: ubiquitin-protein ligase homology <UBI>			F:242-279/Domain: WW repeat homology <WW>			
	Query Match 27 1%; Score 1051.5; DB 2; Length 708;			Query Match 26 4%; Score 1026.5; DB 2; Length 671;			
	Best Local Similarity 36.1%; Pred. No. 2.1e-68;			Best Local Similarity 32.9%; Pred. No. 1.3e-66;			
	Matches 244; Conservative 102; Mismatches 194; Gaps 19;			Mismatches 253; Indels 125; Gaps 18;			
	50 LDPEKHNHYDLYVGKTDTSITISWVHHKTKHRQGAGFLGCVRLISNA-109			Matches 249; Conservative 128; Mismatches 253; Indels 125; Gaps 18;			
>	42 LPGWZERQDV-LGRTYYV---MHEE-----ARTQWKR--70			QY	6 KIRLTVLCAKRNALKDFFRLPDKFALKVWVDDGGQCHSTDVTRNLTDPKWNQHYDLYVGKT	65	
	110 LCKLNPS-----DTDAVRGQIIVVSLQTRDRIGTGGSYVDCRGALLEN-----BGTV 154			Db	7 EVQLTILHVEGLWKGNGLLRSKPYLLISVD-DDQFIKTNVASYGTLRLSWGFTQKTVSPQ	65	
>	71 -----PSDDDDLTDEDIDDMQLQAQBAFTTRQIEBDVCPDNBESPNWEIYREDENTE 125			QY	66 DSITISWVHHKTKHRQGAGFLGCVRLISNA--IISRLKDGTQYQRDLCKLNPSDDAVR	122	
	155 YEDSGPBRPLSCFME-----EP-----PYTDSTGAAAGGG--NCRFVES 192			Db	66 SIIIDASGCAWETRIDEFGHVYYIKSPOLSVISAISHEKLEN-----RSPSGSYR	120	
{	126 YSGQAVQSPPSGRIDYOTHLABEFNTRLAYCGNPAITSQPVTTSSNSRGSLQTCTIFBEQ 185			QY	123 GQIVYSLQTRDRIGTGGSYVDCRGALLENEGTYEDSGPGRPLSCFMEEPAP-----YTD	176	
	193 PSQDORLQAQLRNPDRYRGSQTPQRPHGHOSPELPEGEFORTVQGQYYELHTQTVS 252			Db	121 GSVVLFLKR-----SRKLFPEPADKSQICID	147	
>	186 PTLEVLP-----SSGJPPGMBEKQDRGSYYVDHNSKTT 222			QY	177 SGAAAG-----GGNCNCRFVESP--SQDQRQLQARLRLNPDVRSLSQTPQRPHGHQS	225	
	253 TWHD-----RIPDL-NSVNCDELGP-LPPGMEVRSYSGRIFTYDHNRRTTQFDP 303			Db	148 IIDDASGCAWETRIDEFGHVYYIKSPOLSVISAISHEKLEN-----LTPK-----192		
b	223 TWSRPTMQDDPDRSKIPAHLRGKTDSDLGPUPGWEERTTDGRFFFINNIKTTQWDP 282			QY	226 PELPPEWVRSVSGRIFTYDHNRRTTQFDP-----HDPRIPRDINSYNCDEL	271	
y	304 RLHJMNHQCKLKEPSQDPLPLPSEGSLDEELPAQYERDILVQKXKVLHESLQQPQAG 363			Db	193 -QLKVEFSQ-----PLFNNQSKSSLKINLEYKVTKHLLBYP-LALSVRQQVAVEK	241	
b	283 RLQNY----AIGCPAVP-----YSRDYKRYVEFPERKLKQTDIPN 319			QY	272 GPLPPWEWVRSVSGRIFTYDHNRRTTQFDP-----GDPDNV-----ASDVS	331	
y	364 HCRLRQYRERDLYVOKLKVYKGERBGLDYGSSVARWLYLICHENL 422			Db	242 GPLPAWENPLSDEHYVYDVTQHDTKTTWSDPDNV-----	284	
b	320 KPEMKLRRANILEDSYRR IMGVKRADLIKARIWIEFDGEKGLDYGSSVARWFLISKMF 379			QY	332 DEELPQYRERDLYVOKLKVYKGERBGLDYGSSVARWLYLICHENL 422	39	

285 ENTDSQQINDEYQRKIAMYDRPEMAVNDQ---LQLKVSPATTEDAYDIISKSVSD 341  
 390 LKKRIMVKPFRGEEGIDGGYAREMYLICHEMINPYGELQFYSTDNTMLQINPDSSINP 449  
 342 MTKKLILIRFNEGDIDGYGSREFFYIPLSHAIIFNGISLSEATDDNYGLQISPLSVNP 401  
 450 DHLSTPHFVGRIMGLAVFHGHYINGGFTPVYKOLGKPIQSLSLEVDPELKHSVWIL 509  
 402 DFRSTFRFVRGMGIAIYHRYLDQFLVLPYKRLQPLCLEDVQDVDETYYESKWK 461  
 510 ENDITPVLDTICPVCERNAAGRILQHELKENGRNVPTEENKEYVRLVYNNWERMGIEAQ 569  
 462 NNDVDSLCLNFSVENRFSSESVTDLIPGRNTAVANQNQKMYLKRALTEHKLVTSEEQ 521  
 RESULT 11  
 T37964  
 570 PLALKQGFNLIPQHLLKPPDKELLELIGGLDKIDLAQWKSNTTRLKHCVADSNTIVWFN 629  
 522 ENALKQGLNLNLLPDSVLQINENELDTLNGKRDIVQDWKRTDYSYETTDIVTWIFN 581  
 630 QAVETTDEERBARLLOFVITESTRVLQDGKALQSTTGAGPREFTHIDANTDNPKAH 689  
 582 ELLSERSPPEAKKLQFATGTSRLFSGFKDFMHGSD---GPRKFTIERV-GHISQUPKAH 637  
 690 TCFNRDIPPESYKLYEKULLTAYETTCGFAVE 723  
 638 TCFNRDIPPINSKEPLEQKLUTIA-QETAGFGTE 671

SULT 10  
 9799 Altered to TOM1 protein [imported] - Neurospora crassa  
 Species: Neurospora crassa  
 Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
 Accession: T49799  
 Schulte, U.; Aign, V.; Bohaisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
 Submitted to the Protein Sequence Database, May 2000  
 Reference number: 225022  
 Accession: T49799  
 Status: preliminary  
 Molecule type: DNA  
 Residues: 1-3839 <SCH>  
 Cross-references: EMBL:AL356834; GSPDB:GN00116; NCSP;B11B22..10  
 Experimental source: BAC clone B11B22; strain OR74A  
 Genetics:  
 Gene: NCSP;B11B22..10  
 Map position: 6  
 Introns: 16/3; 2607/1; 2623/1; 2658/1; 2845/1; 2987/2; 3204/3; 3694/1; 3809/1  
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 Y 275 PPGMEVRSTVSGRLI-FVQDHNRRTQFTDPBLHHMMHQCLKEESQPLPSEGSLDE 333  
 3410 PP---EDRIAGLFPTFEHRII-----LNELVRENPKLMSGTESLIVKQPKVLEFD 3458  
 Y 334 ELPAQYRBDLVQKLKVLRHELSLQQPQAGHCRIVYESRETFEEYRQNMKMRPDLK-K 392  
 3459 N-KRNYFTRSVHSKYQQTRHSPPLQ----LQVREHVPHDSFRSLYYKKADELKFG 3510  
 Y 393 RLUVKPFRGEEGIDGGYAREMYLICHEMINPYGELQFYSTDNTMLQINPDSSINPDL 452  
 3511 KLNTRFQGEGVAGGTREWQVLSSQMFEDNYTFVPPVSSDRTTFPHNKLSPINDEHL 3570  
 / 453 SYTFVGRIMGLAVFHGHYINGGFTPVYKOLGKPIQSLSLEVDPELKHSVWILEND 512  
 3571 PFPFPIGRTIGKALYEGRILLECYFSRAVYKRILGKPSVRLMESSDPDYLKSLWMLEND 3630  
 513 ITPLUDTICPVCERNAAGRILQHELKENGRNVPTEENKEYVRLVYNNWERMGIEAQFA 572  
 3631 ITDILITETSVDEIDVFGEVKVDLIEGNGRNIPVTEENKEYVRLITSYRDQMK 3690

Qy 573 LQKGPNELIJPOHLLKPFQKELELILLIGGLDKIDLAQWKSNTTRLKHCVADSNTIVWFNQAV 632  
 Db 3691 FTGCFHRTIPPELIAFNEQUELJISGPIDDDWKRANTEVYNSAGAPOCWFNDAV 3750  
 Qy 633 ETIDDEERBARLLOFVITESTRVLQDGKALQSTTGAGPREFTHIDANTDNPKAHCF 692  
 Db 3751 RSDKEELAKLQFVGTGSKYPLNGFKELGMMGVS--RFNTIRDYGSKDRLFSSTCF 3807  
 Qy 693 NRDIPPESYKLYEKULLTAYETTCGFA 721  
 Db 3808 NQDLPETENYETLRSQQLKAITAGSDYFGFA 3839  
 RESULT 11  
 T37964  
 probable ubiquitin ligase - fission yeast (Schizosaccharomyces pombe)  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 03-Dec-1999 #text\_change 03-Dec-1999  
 C;Accession: T37964  
 R;Author, K.; Charcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.;  
 submitted to the EMBL Data Library, September 1997  
 A;Reference number: T37964  
 A;Accession: T37964  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-3227 <DEV>  
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 A;Map position: 1  
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 Db 2838 LVKNPKVLIBFENKRNYFNQRLHEAAKE-QEPLNITVRRDHFLDSYRALHFKADEVK 2896  
 Qy 392 -KRLMKPFGEGEDYGGYAREMYLICHEMINPYGELQFQSTDNTYMLQINPDSSINPDL 450  
 Db 2897 FSKLNIHFRDEEGYDAGGYTREWQVLARQMPNEDPALFLPVTDGATTFHNRSVNPD 2956  
 Qy 451 HLSYFHVGRIMGLAVFHGHYINGGFTPVYKOLGKPIQSLSLEVDPELKHSVWILE 510  
 Db 2957 HLSYFHKFTRGIIGALYGRLLUCHPSRAVYKMLRSVSYTKDIESLDPDYLKSLWMLN 3016  
 Qy 511 NDITPVLDTFCVBNHAERFLQHELKENGGRNPVTPBENKKEYVRLVNNWFMRGTEBAQF 570  
 Db 3017 NDIDDITEPFAVEKDVGKETVVDLIPNGRNTPVTELKQNYVNRMVYDYLRESYTKDQL 3076  
 Qy 571 LALQGFNELIOPQHLLKPKDQEKEELIIGGLDKIDLAQWKSNTTRLKHCVADSNTIVWFQ 630  
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 Db 3137 AVRSDEEEAKLQFARTSKVPLNGPKELMSGF---QRMNIIKSYGSLARDQSHI 3193  
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 Db 3194 CFNQDLPEYDTQQLRSMLLTAINEGSEGFGEA 3227  
 RESULT 12  
 H96599  
 Protein: P14J16..10 [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C;Accession: He6599  
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Feddespiel, N.A.; Kaul, S.; White, O.; Alone  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Conway, A.B.; Dewar, K

an, N.F.; Hughes, B.; Huizar, L.	
ture 408; Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maii, R.; Marziali, A.; Rooney, T.; Rowley, D.; Sakano, H.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.	
title: Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis</i> . reference number: AB6411; MUID:21016719; PMID:11130712 accession: H96599	
ip position: 1	
ip molecule type: DNA	
cross-references: GB:AE005173; NID:98778329; PIDN:AAF79338.1; GSPDB:GN00141	
genetics: name: P14J16.10	
every Match	20 2%; Score 784; DB 2; Length 4056;
best Local Similarity	39 4%; Pred. No. 9.5e-48;
matches 172; Conservative	65; Mismatches 138; Indels 62; Gaps 7;
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3624 DFDNKAYFRSKIRHDQHSGPRISVRAYEDSTQNLMSPSQDILKGRNVQFG 3693	
401 EEEGLDYGVAEFLWYLICHENLNPVYGLFOYSTNTYMLQINPDSINPDHLSYHFVGR 460	
3684 EEGIDAGGLTIEWQLLSRVIETDKGALLFT-TVGDNATFQDPNPNSYVQTHLSFKVGR 3742	
461 IMGLAYFHGHYINGGETVPEYKQLQKPIQLSDIYDPELHKSLWILENDITPVLDHT 520	
3743 MYAKALDGQOLIDVYFFRSFYKHIGKVTVYHDIATEVDPYKQNRLWLLENDVSSLDT 3802	
521 F----	CVE--HNAGFRGRLQHELKPNGRN 542
3803 PSMDADEKHLIYEKTEVRLMCFCLFWCPIPKCHCIELTLISLMKKVTDYELPPGGRN 38662	
543 VSVTEENKEYVRLYYDNWRFREGIEAFLAQKGPNELIPOLHLKEPDQEKELELIGGLD 602	
3863 IRVTEETKHEYDVLVAGHILTMAIRPQINAFLLEGNELEPLBS1FNDKELELISGLP 3922	
603 KID-----LNDKRSNTLKHCVADSNIVRWWQAVTFDEERRARLQFV 647	
3923 EINDCKLSDIDQYLCAYPLDDIKANTETYSYTAGSPVIIHWNEVKAFAKSFEDMARLQFV 3982	
648 TGSTRVPYQGFKAQGSGTAAGPFLTHLIDANTDNLPKAHTCFRIDPPYESYBKLY 707	
3983 TGSRKVPFLGFKALQ--GISGQRQLQIHKAVGAPERLPSAHTCFNOLDLEYQSKEQLQ 4039	
708 EXLTATAVBETC---GFA 721	
4040 ERLLIAHEASEGGFA 4056	
ULT 13	
491	
Quitin-protein ligase homolog F1707.15 - <i>Arabidopsis thaliana</i>	
Species: <i>Arabidopsis thaliana</i> (mouse-ear cress)	
Accession: T01491	#text_change 04-Mar-2000
Yotsukaiwa, T.S.; Schwarz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Pederspiel, N.	
Submitted to the EMBL Data Library, June 1998	
Description: <i>Arabidopsis thaliana</i> chromosome 1 BAC F1707 sequence.	
Reference number: Z11334	
Accession: T01491	
Status: translated from GB/EMBL/DDJB	
Molecule type: DNA	
Cross references: EMBL:AC003671; NID:g2833627; PID:g3176690; GSPDB:GN00059; ATSP:PI1707	
Experimental source: cultivar Columbia	

486 GRPIQISDLESDVPELHKSLWILLNDITPVLDHTFCVHNAGRLOHELKPGNRPV 545  
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 3033 GRPVSKDMSLDPYKSLWILLNDITDIEEFSVETDDYGEHVKINLIEGGDIIV 3092  
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 546 TEENKREYVRLYVNNRFMRGIEAQFLALQKGFNELIPOHLLKEPFDQEKELELIGGLDKID 605  
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 3093 TEANKQDYVKKVVEYKLQTSVREQMDNFLYGFYALISQDLITFDEQFLELLSGLPDID 3152  
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 606 LNDWKSNTRLKHCVDSNIVRWFWAVETDEERARLQFUTGSTRIPLQCFFKAQGST 665  
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 3153 VDDWQNTTNYNTAATCKEYSVFNAVRSDAEAKLQQFVGTGSKPLNGFKELSGVN 3212  
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 666 GAAGPRLFTIHLIDANTDNLPKAHTTCPRNIDIPPMYESYKLYEKLLTAAVE 716  
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 3213 GVC--XFSIHRDFGSSERLPSHSHTCFNQINLPPYESYETLRSGLLAIN 3260  
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 0274 hypothetical protein F45H7.6 - Caenorhabditis elegans  
 Species: Caenorhabditis elegans  
 Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text\_change 18-Aug-2000  
 Accession: T22257; T22257  
 Percy, C.  
 Submitted to the EMBL Data Library, November 1994.  
 Reference number: Z19245  
 Accession: T20274  
 Status: Preliminary; translated from GB/EMBL/DDBJ  
 Molecule type: DNA  
 Residues: <WIL>  
 Cross-references: EMBL:Z46793; PIDN:CAA86773.1; GSPDB:GN00021; CESP:F45H7.6  
 Experimental source: Clone C56G7  
 Percy, C.  
 Submitted to the EMBL Data Library, June 1994  
 Reference number: Z19538  
 Accession: T22257  
 Status: Preliminary; translated from GB/EMBL/DDBJ  
 Molecule type: DNA  
 Residues: <WT2>  
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 Gene: CESP:F45H7.6  
 :Map position: 3  
 :Introns: 30/3: 54/1: 118/1: 185/2: 213/1: 260/3: 288/2: 353/2: 454/1: 559/2: 642/2: 74  
 /Superfamily: WW repeat homology  
 ;329-267/Domain: WW repeat homology <WW1>  
 ;372-408/Domain: WW repeat homology <WW2>  
 Y Query Match 17.2%; Score 669; DB 2; Length 889;  
 Best local Similarity 28.7%; Prod. No. 2.2e-40;  
 Matches 168; Conservative 104; Mismatches 203; Indels 110; Gaps 15;  
 Y 232 YEQQRTVQGVYFHQTQGVSWHDPPIPRDLN-----SYNCDELGPPLP 276  
 b 322 YENQDAMQ----IYNECSVVZRHAIRHQKLDPPSKFENQPLFVRFVNLFADITQPLPS 376  
 Y 277 GWERSTSGRIVFDNRRTOTFDRRLHHIMNHQCGKPSQPLPBEGS-----329  
 b 377 GWEC-ITMNNRTVFLNHNKEISFYDVRRE---ETKTSGRRGSVPDRSSSTAHKGKI 430  
 Y 330 -----IEDEELP--AQRYERDLV-----345  
 b 431 DHALSKECDLKRIAQDNFPQIAERISKLMJIERFGGLAVASLANDDTLANSMDSN 490  
 Y 346 -----QKLKVLRHLSLQQPAQGHCR-----EVSRREEFEESYRQIMKMRPKDQLKK-RL 394  
 b 491 TEKLAGEGDNIKMYYEDMKKEKLGKGPRLCKVSRRLDDAFAIRILNVDPFVLRKSRL 550  
 Y 395 MKRDFGEGLGDYGWAREYLILCHEMLNPYQFYSTONIYMLQINPDESINDHSLY 454  
 b 551 HIRPGELALDYGGSREPFILSRELPHPKNGYFEYE-GNDYHQLRPRCCETEKEKWW 609

455 FHIVGRIMGLAVPHGYINGPPTVPPKQOLLGKPTQOLSDLESVPDELKSLVWILENDIT 514  
 QY 610 LILGGRVLALAVHRCIDVFFTNVFKSLQKRPVTILMDPKESDAFBYKSMNNVILENDVV 669  
 Db 515 PVDLHTFCVBEHNFGR-----LQHELKPGNRPVTEBNKKEYTYRLYN 559  
 QY 670 D-LEMSPVYSSMTNGKYSQDLTLLSIVSVALQAEQELVPGESQMVTEANKAEOFIDLMCQ 728  
 QY 560 WRFERGIEQFLLQKGFNELLPHQILKPFQDKELELLIGLDKIDLNDWIKSNPLRKHV 619  
 Db 729 KCAARGVEKPLELLTSNQILNDNLINSLESSDLKRILGSSLDELDNDWRTNTIYKGGY 783  
 QY 620 ADSNI-VERMWOAVETFDEERRALIQFVGSTRVPLQGKZALQGSTGAAGPRLTHL 678  
 Db 789 SDCHIVVFWEITMNTQNEDFLVTSSTVPEFGFALARNEEIS--XFCIEKW 845  
 QY 679 DANDNLPKAHTCFNRIDIPPMYESYKLYEKLLTAAVEBTCTGFAVE 723  
 Db 846 -GDATSFPAHTCENRLOLQPSNTKQOLSKLQQAIVNGMSIE 889

Search completed: February 20, 2004, 15:26:53  
 Job time : 20.2026 secs

GenCore version 5.1.6						
Copyright (c) 1993 - 2004 Compugen Ltd.						
protein - protein search, using sw model						
on:	February 20, 2004, 15:25:26	: Search time 10.8131 Seconds				
		(without alignments)				
		3144.377 Million cell updates/sec				
RefId:	US-10-009-945-2					
Effect score:	3884					
Sequence:	1 GASSIKIRLTVICAKNLAKK.....EKLYKEKLITAVEETCGFAVE 723					
String table:	BLOSUM62					
	GapOp 10.0 , GapExt 0.5					
Searched:	127863 seqs, 47026705 residues					
Initial number of hits satisfying chosen parameters:	127863					
Maximum DB seq length: 0						
Minimum DB seq length: 2000000000						
t-processing: Minimum Match 0%						
	Maximum Match 100%					
	Listing first 45 summaries					
Database :	SwissProt 41.1*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.						
SUMMARIES						
	%					
Result	Query	Match	Length	DB	ID	Description
1	3855	99.3	757	1	SIF1_HUMAN	Q9ne7 homo sapiens
2	3548	91.3	731	1	SDF1_XENLA	Q9pan2 xenopus laevis
3	3229.5	83.7	619	1	SDF1_MOUSE	Q9eqm6 mus musculus
4	3001	77.3	748	1	SDF2_HUMAN	Q9ha4 homo sapiens
5	1492.5	38.4	767	1	P0B12_SCHPO	Q92462 schizosaccharomyces pombe
6	1377	35.5	809	1	RASF5_YEAST	P39940 saccharomyces cerevisiae
7	1259	32.4	927	1	NED4_HUMAN	P46334 homo sapiens
8	1225	31.5	957	1	NED4_MOUSE	P46335 mus musculus
9	627.5	16.2	870	1	TRB1_RAT	P51153 rattus norvegicus
10	53.4	13.7	875	1	UB3A_HUMAN	P05086 homo sapiens
11	48.3	12.4	885	1	UB3A_MOUSE	P08759 mus musculus
12	48.3	12.4	892	1	HDL4_YEAST	P40935 saccharomyces cerevisiae
13	44.9	11.6	1050	1	HER3_HUMAN	Q15043 homo sapiens
14	35.8	9.2	1992	1	TRIB1_HUMAN	Q14639 homo sapiens
15	3.54	9.1	910	1	HDL5_YEAST	P53119 saccharomyces cerevisiae
16	278.5	7.2	2799	1	EDD_HUMAN	P05071 homo sapiens
17	227.7	7.1	920	1	EDD_RAT	P02651 rat
18	262.15	6.8	1483	1	UPF4_YEAST	P33223 saccharomyces cerevisiae
19	257	6.6	1647	1	YDF1_SCHPO	P10435 caenorhabditis elegans
20	238.5	6.1	472	1	YAP1_MOUSE	P46938 mus musculus
21	238.5	6.1	1620	1	HEJ1_HUMAN	P05119 drosophila melanogaster
22	222	5.7	295	1	HYD_DRONE	P46936 gallus gallus
23	161.2	4.2	448	1	YAPT1_CHICK	P46937 homo sapiens
24	161.5	4.2	448	1	YAP1_HUMAN	P46938 caenorhabditis elegans
25	12.8	3.3	1813	1	UNI13_CABEL	P27715 caenorhabditis elegans
26	11.9	3.1	575	1	BAG3_HUMAN	P05117 homo sapiens
27	11.6	3.0	577	1	BAG3_MOUSE	P05116 mus musculus
28	11.5	2.9	826	1	RISG5_HUMAN	P043314 homo sapiens
29	11.4	2.9	593	1	CNE5_HUMAN	P09hc33 homo sapiens
30	11.3	2.9	1021	1	YP177_CABEL	P41885 caenorhabditis elegans
31	11.15	2.9	672	1	KPCA_HUMAN	P17282 homo sapiens
32	11.15	2.9	672	1	KPCA_RABIT	P05626 oryctolagus cuniculus
33	11.15	2.9	672	1	KPCA_PAT	P05625 patagonian trout

34	111.5	2.9	5147	1	PCLQ HUMAN	Q9Y670	homo sapien
35	110.5	2.8	597	1	IXR1 YEAST	P33417	saccharomyces cerevisiae
36	110	2.8	658	1	KPC1_HUMAN	Q25378	echinid
37	109.5	2.8	537	1	CNE3_HUMAN	Q75131	homo sapien
38	109	2.8	694	1	RP3A_HUMAN	Q9y210	homo sapien
39	109	2.8	704	1	RP3A_BOVINE	Q06846	bos taurus
40	109	2.8	915	1	PDB2_BRATH	Q23078	arbidopsis thaliana
41	108	2.8	506	1	PYCA_ARCFUL	Q30119	archaeoglobus fulgidus
42	108	2.8	665	1	RNR2_LACLA	Q02246	lactococcus lactis
43	108	2.8	1013	1	PTPX_MACNE	Q02695	macaca nemestrina
44	108	2.8	1178	1	PYC_MOUSE	Q05920	mus musculus
45	108	2.8	5120	1	PCLQ_CHICK	Q9P336	gallus gallus
ALIGNMENTS							
RESULT 1							
SUP1_HUMAN	ID	SUP1_HUMAN	STANDARD;	PRT;	757 AA.		
AC	Q9HC7E; OTS853; Q9UUT8;						
DT	28-FEB-2003 (Rel. 41, Created)						
DT	28-FEB-2003 (Rel. 41, Last sequence update)						
DT	28-FEB-2003 (Rel. 41, Last annotation update)						
DE	Smad ubiquitination regulatory factor 1 (EC 6.3.2.-) (Ubiquitin--protein ligase SMURF1) (Smad-specific E3 ubiquitin ligase 1)						
DE	(SMURF1).						
GN	SMURF1 OR KIAA1625.						
OS	Homo sapiens (Human);						
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OX	NCBI_TAXID=9606;						
RN	[1]						
RP	SEQUENCE OF 10-731 FROM N.A. (ISOFORM SHORT).						
RX	MEDLINE=99385348; PubMed=10458166;						
RA	Zhu H., Kavak S., Abdollahi S., Wrana J.L., Thomsen G.H.;						
RT	"A SWAD ubiquitin ligase targets the BMP pathway and affects embryonic pattern formation."						
RT	Nature 400:687-693 (1999).						
RN	[2]						
RP	SEQUENCE OF 20-731 FROM N.A. (ISOFORM SHORT).						
RA	Stoneking P., Bauer C., O'Neal D.'						
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.						
RN	[3]						
RP	SEQUENCE FROM N.A. (ISOFORM LONG).						
RC	TISSUE-BRAIN;						
RX	MEDLINE=2050683; PubMed=10997877;						
RA	Nagase T., Kikuno R., Nakayama M., Hiroseawa M., Ohara O.;						
RT	"Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."						
RT	DNA Res. 7:173-181 (2000).						
CC	-1 FUNCTION: INTERACTS WITH RECEPTOR-REGULATED SMADS SPECIFIC FOR THE BMP PATHWAY (SMAD1 AND SMAD5) IN ORDER TO TRIGGER THEIR INTEGRATION.						
CC	-1 ALTERNATIVE PRODUCTS:						
CC	Event=Alternative splicing; Named isoforms=2;						
CC	Name=Long;						
CC	Isoid=Q9HC7-1; Sequence=VSP 006812;						
CC	-1 SIMILARITY: Contains 1 C2 domain.						
CC	-1 SIMILARITY: Contains 2 WW domains.						
CC	-1 SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.						
CC	This SRS/PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch">http://www.isb-sib.ch</a> ) or send an email to license@isb-sib.ch).						

EMBL; AP19934; AAC08298.2; -.	430 VKFRGEGLDYGGVAREWLYLCHEMLNPNPYGLFQYSTNDNIMQLQINPDSSTNPDLHLSYF 489
EMBL; AB046845; BAB13434.1; -.	456 HFVGRINGLAVFHGYINGOPTVRYKOLICKRQLSLESDYSPFLPHKSILWILENDITP 515
HSSP; AB046845; BAB13451.1; ALT_INIT.	490 HFVGRIMGLAVFHGYINGOPTVRYKOLICKRQLSLESDYSPFLPHKSILWILENDITP 549
MIM; 605568; -.	516 VLDHIFPCVNEANAPGRILQHLPGRNPVTEENKEYRLYNNWRMRCIBAQFLALQK 575
GO; GO:0005622; C:intracellular; TAS.	550 VLDHIFPCVNEANAPGRILQHLPGRNPVTEENKEYRLYNNWRMRCIBAQFLALQK 609
GO; GO:000211; P:protein degradation, tagging activity; IDA.	576 GFNELLPOHLIKPFDQKELEIIGLKDIDMKNSNTRLKHCVADSNIYRVMFWQAVETP 635
GO; GO:0030154; P:ubiquitin protein ligase activity; IDA.	576 GFNELLPOHLIKPFDQKELEIIGLKDIDMKNSNTRLKHCVADSNIYRVMFWQAVETP 635
GO; GO:0030514; P:ectoderm development; TMS.	610 GFNELLPOHLIKPFDQKELEIIGLKDIDMKNSNTRLKHCVADSNIYRVMFWQAVETP 669
GO; GO:0006464; P:protein modification; TAS.	636 DEERRARLLQFVTGSTRVPLQGFKALQGSTGAAGPRFLTHILIDANTNLPIAHTCNR 695
IntParPro; IPRO000008; C2.	670 DEERRARLLQFVTGSTRVPLQGFKALQGSTGAAGPRFLTHILIDANTNLPIAHTCNR 729
InterPro; IPR000589; HECT_domain.	696 DIPPYESEYKLYEKULLTAYETCGFAVE 723
InterPro; IPR001202; WW_R�ps_WWP.	730 DIPPYESEYKLYEKULLTAYETCGFAVE 757
Pfam; PF00168; C2; 1.	
Pfam; PF00632; HECT; 1.	
Pfam; PF00397; WW; 2.	
SMART; SN00233; C2; 1.	
SMART; SNO0119; HECTC; 1.	
SMART; SNO0456; WW; 2.	
PROSITE; PS00459; C2 DOMAIN; 1.	
PROSITE; PS00004; C2 DOMAIN; 1.	
PROSITE; PS50037; HECT; 1.	
PROSITE; PS01159; WW DOMAIN; 1.	
UBL conjugation pathway; Li-Gase; Repeat; Alternative splicing.	
DOMAIN 1 99 C2 DOMAIN.	
DOMAIN 1 267 WW 1.	
DOMAIN 1 339 WW 2.	
DOMAIN 1 420 757 HECT.	
BINDING 725 UBIQUITIN.	
VARSPLIC 269 294 Missing (in isoform Short).	
MUTAGEN 725 /Frid=VSP 006812.	
SEQUENCE 757 AA; 86113 MW; 8917171FC47B40E9 CRC64;	
Query Match 99.3%; Score 3855; DB 1; Length 757;	
Best Local Similarity 96.5%; Pred. No. 8.8e-2/2;	
Matches 722; Conservative 0; Mis matches 0; Indels 26; Gaps 1;	
2 GSSSIKRITVJCAALKDFFRDLDPFAKIVDGGSGOCHSPTDVNTLDPKRNQHDYD 61	
10 GSSSIKRITVJCAALKDFFRDLDPFAKIVDGGSGOCHSPTDVNTLDPKRNQHDYD 69	
62 VGTIDTISWNHKKHHKQGFLGCVLNSAISLKDTCYQRIDLCKLNPSSTDVA 121	
70 VGTIDTISWNHKKHHKQGFLGCVLNSAISLKDTCYQRIDLCKLNPSSTDVA 129	
122 RQOTIVSLQDRIGGGSYVDCRCLLENEGTYEDSGSPGRPLSCMEEPAFTDTGAA 181	
130 RQTRIVSLQDRIGGGSYVDCRCLLENEGTVFEDSGSPGRPLSCMEEPAFTDTGAA 189	
182 AGGGNCRFVESPQDORLQLAQRLNPDYRGSLQPQNRPFGHOSPELGEYORTVQGQ 241	
190 AGGGNCRFVESPQDORLQLAQRLNPDYRGSLQPQNRPFGHOSPELGEYORTVQGQ 249	
242 VYFLHFTQTCSTWHBRI-----PRDINSYNCDEGLPLP 275	
250 VYFLHFTQTCSTWHBRI-----PRDINSYNCDEGLPLP 309	
276 PWEEVSTSVSRIYFDHNRTTQTDPRLEHTNHCOLKERSQPLPLPSGSLSDEEL 335	
310 PWEEVSTSVSRIYFDHNRTTQTDPRLEHTNHCOLKERSQPLPLPSGSLSDEEL 369	
336 PAQRYERDLVOKLKVRLHELSLQQQAGHRIEVSREPEESYRQIMKMRPKDLKRLM 395	
370 PAQRYERDLVOKLKVRLHELSLQQQAGHRIEVSREPEESYRQIMKMRPKDLKRLM 429	
396 VKFRGEGLDYGGVAREWLYLCHEMLNPNPYGLFQYSTNDNIMQLQINPDSSTNPDLHLSYF 455	

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Db QY 456 HFVGRINGLAVFHGYINGOPTVRYKOLICKRQLSLESDYSPFLPHKSILWILENDITP 515

Db QY 490 HFVGRIMGLAVFHGYINGOPTVRYKOLICKRQLSLESDYSPFLPHKSILWILENDITP 549

Db QY 516 VLDHIFPCVNEANAPGRILQHLPGRNPVTEENKEYRLYNNWRMRCIBAQFLALQK 575

Db QY 550 VLDHIFPCVNEANAPGRILQHLPGRNPVTEENKEYRLYNNWRMRCIBAQFLALQK 609

Db QY 576 GFNELLPOHLIKPFDQKELEIIGLKDIDMKNSNTRLKHCVADSNIYRVMFWQAVETP 635

Db QY 610 GFNELLPOHLIKPFDQKELEIIGLKDIDMKNSNTRLKHCVADSNIYRVMFWQAVETP 669

Db QY 636 DEERRARLLQFVTGSTRVPLQGFKALQGSTGAAGPRFLTHILIDANTNLPIAHTCNR 695

Db QY 670 DEERRARLLQFVTGSTRVPLQGFKALQGSTGAAGPRFLTHILIDANTNLPIAHTCNR 729

Db QY 696 DIPPYESEYKLYEKULLTAYETCGFAVE 723

Db QY 730 DIPPYESEYKLYEKULLTAYETCGFAVE 757

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RESULT 2

SUR1\_XENLA STANDARD PROT; 731 AA.

ID\_SUF1\_XENLA ID\_SUF1\_XENLA

AC\_QPPJN2\_ AC\_QPPJN2\_

DT\_28-FEB-2003 (Rel. 41, Created)

DT\_28-FEB-2003 (Rel. 41, Last sequence update)

DT\_28-FEB-2003 (Rel. 41, Last annotation update)

DB\_Smad ubiquitination regulatory factor 1 (EC 6.3.2.-) (Ubiquitin-regulatory factor 1) (XSMURF1). Protein ligase SMURF1 (Smad-specific E3 ubiquitin ligase) (XSMURF1).

GN\_SMURF1.

OS\_Xenopus laevis (African Clawed frog).

OC\_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC\_Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopoda; Xenopus.

NCBI\_TAXID=8355; RN [1]

RP\_SEQUENCE FROM N.A.

RC\_TISSUE-Blaula; RC\_TISSUE-Blaula;

RX\_MEDLINE=9935348; RX\_MEDLINE=10458166;

RA\_Zhu H.; Kavak P.; Abdollahi S.; Wana J.L.; Thomsen G.H.; RT "A SMAD ubiquitin ligase targets the BMP pathway and affects embryonic pattern formation." RL\_Nature 400:687-693 (1999).

CC\_- FUNCTION: interacts with receptor-regulated SMADs specific for the BMP pathway (SMAD1 and SMAD5) in order to trigger their ubiquitination and degradation and hence their inactivation. May regulate ectodermal differentiation and pattern by modulating BMP signaling and may enhance cellular responsiveness to the SMAD2 (activin/TGF-BETA) pathway.

CC\_- DEVELOPMENTAL STAGE: expressed from the egg stage to the swimming tadpole with maximum levels observed in the stages from egg to gastrula. At gastrulation distributed uniformly in embryonic ectoderm and involving mesoderm, and expression gradually localizes to the nervous system, at early tadpole stages expressed in the CNS, eye, branchial arches, kidney and somites.

CC\_- SIMILARITY: Contains 1 C2 domain.

CC\_- SIMILARITY: Contains 2 WW domains.

CC\_- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.

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DR\_EMBL; AF169310; AAD52564.1; -

DR\_GO; GO:0005622; C:intraceillar; TAS.

GO; GO:0000211; F:protein degradation tagging activity; IDA.  
 GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.  
 GO; GO:0007398; P:cell differentiation; TAS.  
 GO; GO:0030514; P:ecdysteroid development; TAS.  
 GO; GO:00464; P:negative regulation of BMP signaling pathway; TAS.  
 GO; GO:0006512; P:ubiquitin modification; TAS.  
 InterPro; IPR000008; C2; InterPro; IPR000569; HECT domain.  
 InterPro; IPR001202; WW\_Rsp5\_WWP.  
 Pfam; PF00168; C2; 1.  
 Pfam; PF00532; HECT; 1.  
 Pfam; PF00397; WW; 2.  
 SMART; SM00023; C2; 1.  
 SMART; SM00119; HECTC; 1.  
 SMART; SM00456; WW; 2.  
 PROSITE; PS00493; C2 DOMAIN\_1; 1.  
 PROSITE; PS50004; C2 DOMAIN\_2; 1.  
 PROSITE; PS50237; HECT; 1.  
 PROSITE; PS01159; WW DOMAIN\_1; 1.  
 PROSITE; PS50020; WW DOMAIN\_2; 1.  
 Ubiquitination Pathway; Ligase; Repeat.  
 DOMAIN 1 99 C2 DOMAIN.  
 DOMAIN 233 266 WW 1.  
 DOMAIN 279 312 WW 2.  
 DOMAIN 394 731 HECT.  
 SEQUENCE 731 AA; 83259 MW; 3CB38E512A42CE2C CRC64;

Query Match 91.3%; Score 3548; DB 1; Length 731;  
 Best Local Similarity 91.0%; Pred. No. 1.5e-249;  
 Matches 659; Conservative 34; Mismatches 29; Indexes 2; Gaps 2;

1	GESSIKRPLTVCAKNLANKDFRFLDPFKAKIVDGGSOCHSDPTVQTLDPKWQHNDL	60
2	GSSSIRVRLTVLCAKNLAKRKFRRFLDPFKAKIVDGGSOCHSDPTVQTLDPKWQHNDL	68
3	YVSKTDSITISWNNHKCHHKQGAGFEGCVRLSNASISRLKDTGYQYRDLCKLNPTND	120
4	YVSKMDSITISWNNHKTHHKQGAGFEGCVRLSNASISRLKDTGYQYRDLCKLNPTND	128
5	VRCQIVVSLQTDRIGTGTGSYDVRGLILENEGTYYEDSGFGRPLSCFMFRPAPTDSTGA	180
6	VRCQIVVSLQTDRIGTGTGSYDVRGLILENEGTYYEDSGFGRPLSCFMFRPAPTDGF-	187
7	AAGGNCNRFVEESPQDORLQARLNPDVGRSLCPQNRPFGHOSPELPEGYFRTVQG	240
8	AAGGPNPGLVSEGGQEBRVLQARVREPEVSHVQPQNRSRGFQODLEGYFRTVQG	247
9	QVXFILHTOTGVSTWHDPRIQLNSYNCDLGPGWERTYTSGRITYFDHNRRTQF	300
10	QVXFILHTOTGVSTWHDPRIQLNSYNCDLGPGWERTYTSGRITYFDHNRRTQF	307
11	TDPRLHHIMMHQCQLEPSQPLPSEGSLD-EELPAQRYERDVKLKVHLHSQQ	359
12	TDPRLHHIINHQSQLKEPNHALPVQDSGUDGDPFAQYERDVKLKVHLHSQQ	367
13	PQAGHCRLEVSREBIEFSYRQTMKRPDKLKKRNVKFGEEGIDGVAREMLYLICH	419
14	PQAGHCRVEVSREEIFESYRQTMKRPDKLKKRNVKFGEEGIDGVAREMLYLICH	427
15	EMNPYGFQYSTDNTYMLQINPDDSSINPDHLSFHVGrimGAVFHGHYINGFIVP	479
16	EMNPYGFQYSTDNTYMLQINPDDSSINPDHLSFHVGrimGAVFHGHYINGFIVP	487
17	FYCKLGPQIQLSLESDPHEKSLWILNDPTEVCFYHAGTQFQKELBLIG	539
18	FYCKLGPQIQLSLESDPHEKSLWILNDPTEVCFYHAGTQFQKELBLIG	547
19	GRNPYTFENKKEYVRLYVNAFMRMGEIAQFLALQKGFLIPOLHLKPFQKELBLIG	599
20	GRNPYTFENKKEYVRLYVNAFMRMGEIAQFLALQKGFLIPOLHLKPFQKELBLIG	607
21	GRNPYTFENKKEYVRLYVNAFMRMGEIAQFLALQKGFLIPOLHLKPFQKELBLIG	659

RESULT 3  
 SUFI MOUSE STANDARD; PRT: 619 AA.  
 ID SUFI MOUSE  
 AC Q9C7N6; DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 RA Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Harai A., Fukunishi Y., Konno H., Adachi J., Futuda S., Aizawa K., Iizawa M., Nishi K., Miyasawa H., Kondo S., Yamamoto I., Saito R., Saito T., Okazaki M., Gotohori T., Bono H., Kasukawa T., Matsuda H.A., Ashburner M., Battalov S., Casavant T., Kadota K., Matsuda H.A., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baladarelli P., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Montbairat P., Nordone P., Ring B., Rangwala M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibara Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; RT Functional annotation of a full-length mouse cDNA collection.; RL Nature 405:685-690 (2000).  
 CC -!- FUNCTION: INTERACTS WITH RECEPTOR-REGULATED SMAD5 SPECIFIC FOR THE BMP PATHWAY (SMAD1 AND SMAD5) IN ORDER TO TRIGGER THEIR INACTIVATION (By Ubiquitination and Degradation) AND HENCE THEIR INACTIVATION (By Ubiquitination and Degradation).  
 CC -!- SIMILARITY: Contains 1 C2 domain.  
 CC -!- SIMILARITY: Contains 2 WW domain.  
 CC -!- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.

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CC -!- DR AK015264; BAB29770; 1.  
 CC -!- DR F5SP; Q11526; 1.PIN.  
 CC -!- DR MG1:1923038; 493031ELIORIK.  
 CC -!- DR GO; GO:0005622; Cintiatelular; ISS.  
 CC -!- DR GO; GO:0000211; F:protein degradation tagging activity; ISS.

Db 608 GLDXDISDWKANTRLKHCLANSITVQFWQAVEDEERRARLQFVTGSTRVPLQGFK 667  
 Qy 660 ALQGSTGAAAGPRLFTHILIDANTDNLPKAHTCFNRIDIPPEYESKRYLYKULTAVEETCG 719  
 Db 668 ALQGSTGAAAGPRLFTHILIDANTDNLPKAHTCFNRIDIPPEYESKRYLYKULTAVEETSG 727  
 Qy 720 FAYE 723  
 Db 728 FAYE 731  
 RESULT 3  
 SUFI MOUSE STANDARD; PRT: 619 AA.  
 ID SUFI MOUSE  
 AC Q9C7N6; DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 RA Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Harai A., Fukunishi Y., Konno H., Adachi J., Futuda S., Aizawa K., Iizawa M., Nishi K., Miyasawa H., Kondo S., Yamamoto I., Saito R., Saito T., Okazaki M., Gotohori T., Bono H., Kasukawa T., Matsuda H.A., Ashburner M., Battalov S., Casavant T., Kadota K., Matsuda H.A., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baladarelli P., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Montbairat P., Nordone P., Ring B., Rangwala M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibara Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; RT Functional annotation of a full-length mouse cDNA collection.; RL Nature 405:685-690 (2000).  
 CC -!- FUNCTION: INTERACTS WITH RECEPTOR-REGULATED SMAD5 SPECIFIC FOR THE BMP PATHWAY (SMAD1 AND SMAD5) IN ORDER TO TRIGGER THEIR INACTIVATION (By Ubiquitination and Degradation) AND HENCE THEIR INACTIVATION (By Ubiquitination and Degradation).  
 CC -!- SIMILARITY: Contains 1 C2 domain.  
 CC -!- SIMILARITY: Contains 2 WW domain.  
 CC -!- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.

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CC -!- DR AK015264; BAB29770; 1.  
 CC -!- DR F5SP; Q11526; 1.PIN.  
 CC -!- DR MG1:1923038; 493031ELIORIK.  
 CC -!- DR GO; GO:0005622; Cintiatelular; ISS.  
 CC -!- DR GO; GO:0000211; F:protein degradation tagging activity; ISS.

GO; GO:0004842; Ubiquitin-protein ligase activity; ISS.  
 GO; GO:0030155; Picell differentiation; ISS.  
 GO; GO:003054; Plectoderm development; ISS.  
 GO; GO:0006456; Negative regulation of BMP signaling pathway; ISS.  
 GO; GO:0006514; Protein modification; ISS.  
 InterPro; IPR000085; C2.  
 InterPro; IPR00059; HECT domain.  
 Pfam; PF00632; HECT; 1.  
 Pfam; PF00397; WW; 2.  
 SMART; SM00119; HECT; 1.  
 PROSITE; PS00459; C2\_DOMAIN\_1; PARTIAL.  
 PROSITE; PS50004; C2\_DOMAIN\_2; PARTIAL.  
 PROSITE; PS50337; HECT; 1.  
 PROSITE; PS50159; WW; DOMAIN\_1; 1.  
 PROSITE; PS50020; WW\_DOMAIN\_2; 2.  
 Ub1 conjugation pathway; Ligase; Repeat.  
 NON\_TBR 1  
 DOMAIN 125 158 WW 1.  
 DOMAIN 171 204 WW 2.  
 DOMAIN 619 619 HECT.  
 DOMAIN 35 38 POLY-GLY.  
 SEQUENCE 619 AA; 70902 MW; 4CBE2F5624A7B525 CRC64;  
 Query Match 83.7%; Score 3249.5; DB 1; Length 619;  
 Best Local Similarity 97.3%; Pred. No. 5.le-228; Indels 3; Gaps 1;  
 Matches 605; Conservative 6; Mismatches 8;  
 102 DTGYQIDLKCKLNPSDTDAVQIWTGTVPSLQRDRIGTGSVVDRLNEGTVYESGPG 161  
 1 DTGYQIDLKCKLNPSDTDAVQIWTGTVPSLQRDRIGGGSVVDCRGLLENEGVYESGPG 60  
 162 RPLSCMEEPAPYTDSTGAAAGGNCRFVESPQDQRLOAQQLRNPDVYGSLOTPQNRP 221  
 61 RPLSCMEEPAPYTDGTGAAAGGNCRFVESPQDQRLOQVLPNPEVQGPQTPQNRP 120  
 222 GHQSPELPEGVBQRTVQGQYYFLHTQTCGYSWHDPIPRDLSVNCDELGLPPMVEVR 281  
 121 GHQSPELPEGVBQRTVQGQYYFLHTQTCGYSWHDPIPRDLSVNCDELGLPPMVEVR 180  
 282 STVSGRIFTYFDHNRRTQFTDPRLHIMNHQCOLKPEPSQPLPUSSEGSLEDELPAPORYE 341  
 181 STVSGRIFTYFDHNRRTQFTDPRLHIMNHQCOLKPEPSQPLQPNEGSVEDELPAPORYE 240  
 342 RDIVQKLVLHLSSQPOQAGHCRIEVSSEEFFESYRQIMMRPDQLKRLMVVERGE 401  
 241 RDIVQKLVLHLSSQPOQAGHCRIEVSSEEFFESYRQIMMRPDQLKRLMVVERGE 300  
 402 EGIDYGGVAREWLYLCHEMINPYGLFQYSTNDIYMLQINPDSSINPDHSYFHFYGR 461  
 301 EGDYGGVAREWLYLCHEMINPYGLFQYSTNDIYMLQINPDSSINPDHSYFHFYGR 360  
 462 MGIAVFGHGYINGFTVFKOLLGKPIQSLDLEVDPELHKSLWILENDITPVLDHTF 521  
 361 MGIAVFGHGYINGFTVFKOLLGKPIQSLDLESVDPELHKSLWILENDITPVLDHTF 420  
 522 CYBNHAFRILQHKLKGNGRATPVBNKKEYVRYLYVNRFMRCIEAFLQXGFNELI 581  
 421 CYBNHAFRILQHKLKGNGRATPVBNKKEYVRYLYVNRFMRCIEAFLQXGFNELI 480  
 582 PQHDLKPQDKKELELIGGLDKIDNDWKSNTRLKHCVADSNTYRVWQAVTFDEERRA 641  
 481 PQHDLKPQDKKELELIGGLDKIDNDWKSNTRLKHCVADSNTYRVWQAVTFDEERRA 540  
 642 RLQFVFTGSTRVPLQGPKALQGCGTGAAPRLFTIHLIDANTDNLPKAHTCFNRIDIPYE 701  
 541 RLQFVFTGSTRVPLQGPKALQ--GAGGPRLFITIHLIDANTDNLPKAHTCFNRIDIPYE 597  
 702 SYEWKLYLLTVAETFCFAVE 723  
 598 SYEWKLYLLTVAETFCFAVE 619

RESULT 4  
 SDF2\_HUMAN STANDARD; PRT; 748 AA.  
 ID SDF2\_HUMAN\_QSH260; AC QSH260; DT 28-FEB-2003 (Rel. 41, Created)  
 AC QSH260; DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Smad ubiquitination regulatory factor 2 (EC 6.3.2.-) (Ubiquitin--protein ligase SMURF2) (Smad-specific E3 ubiquitin ligase 2)  
 DE (SMURF2).  
 GN SMURF2.  
 OS Homo sapiens (Human).  
 OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TAXID9606; OX [1]  
 RN SEQUENCE FROM N.A., AND MUTAGENESIS OF PRO-251--VAL-284 AND GLY-297--LEU-330.  
 RP PubMed:116210; RX Kavvaki P., Rasmussen R.K., Causing C.G., Bonni S., Zhu H., RA Thomsen G.H., Wranne J.L.; RT "Smad7 binds to Smurf2 to form an E3 ubiquitin ligase that targets the TGF- $\beta$  receptor for degradation." RL Mol. Cell. 6:1365-1375(2000).  
 RN [2]  
 RN SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-716.  
 RP PubMed:20538422; RX Lin X., Liang M., Peng X.-H., RA Deryck R.; RT "Smad7 is a ubiquitin E3 ligase mediating proteasome-dependent degradation of Smad2 in transforming growth factor- $\beta$  signaling." RL J. Biol. Chem. 275:36818-36822(2000).  
 RN [3]  
 RN SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-716.  
 RP PubMed:21107655; RX Zhang Y., Chang C., Gehling D.J., Hemmati-Brivanlou A., Deryck R.; RT "Regulation of Smad degradation and activity by Smurf2," an E3 protein." RL Proc. Natl. Acad. Sci. U.S.A. 98:974-979(2001).  
 CC -!!- FUNCTION: Interacts with SMAD1, SMAD2 and SMAD7 in order to trigger their ubiquitination and proteasome-dependent degradation.  
 CC Enhances the inhibitory activity of SMAD2 and reduces the transcriptional activity of SMAD2. Coexpression of SMTRF2 with SMAD1 results in considerable decrease in steady-state level of SMAD1 protein and a smaller decrease of SMAD7 level.  
 CC -!!- SUBUNIT: Interacts with SMAD1, SMAD2, SMAD3, SMAD6 and SMAD7 but not SMAD4.  
 CC -!!- SUBCELLULAR LOCATION: Nuclear. Cytoplasmic in the presence of SMAD7.  
 CC -!!- TISSUE SPECIFICITY: Widely expressed.  
 CC -!!- DOMAIN: The second and third WW domains are responsible for interaction with R-SMAD (SMAD1, SMAD2 and SMAD3).  
 CC -!!- SIMILARITY: Contains 1 C2 domain.  
 CC -!!- SIMILARITY: Contains 3 WW domains.  
 CC -!!- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.  
 CC -!!- DOMAIN: The ENBL outstation - This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for Commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  
 CC -!!- DOMAIN: AF110676; AAG45322.1; DR EMBL; AF01463; AAG25341.1; DR EMBL; AY01418; AAG50421.1; DR HSSP; Q15256; 1PIN.  
 GO; GO:0004842; Ubiquitin-protein ligase activity; NAS.  
 GO; GO:0016481; P:negative regulation of transcription; NAS.

RESULT 5	
PUB1	SCHPO
ID	PUB1_SCHPO STANDARD; PRY; 767 AA.
AC	Q92162; O14454;
DT	01-NOV-1997 (Rel. 35, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ubiquitin-protein ligase pubi (EC 6.3.2.-).
GN	Publ OR SPAC11G7_02.
OS	Schizosaccharomyces pombe (Fission yeast).
OC	Fungi; Ascomycota; Schizosaccharomycetes;
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;
OC	Schizosaccharomyces.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96205868; PubMed=8635463;
RA	Nefsky B., Beach D.,
RT	"Publ acts as an E6-AP-like protein ubiquitin ligase in the degradation of Cdc25."
RT	EMBO J. 15:1301-1312(1996).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=227
RX	MEDLINE=97340937; PubMed=9197411;
RA	Salchi R., Jia Z., Karagiannis J., Young P. G.;
RT	"tolerance of low pH in Schizosaccharomyces Pombe requires a functioning pub1 ubiquitin ligase."
RL	Mol. Gen. Genet. 254:520-528(1997).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=972;
RX	MEDLINE=21848401; PubMed=11853360;
RA	Wood V., Gwilliam R., Rayjandream M.A., Lyne M., Lyne R., Stewart A.,
RA	Sgourou J., Peat N., Rayles J., Baker S., Basham D., Bowman S.,
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA	Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jages K.,
RA	James K., Jones L., Jones M., Leathur S., McDonald S., McLean J.,
RA	Mooney P., Moule S., Mungall K., Murphy L., Neale D., Odell C.,
RA	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitz E.,
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA	Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Whitehead S.,
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA	Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA	Weltiens I., Vansbreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA	Borzym K., Langer T., Beck C., Lehrer H., Moestl D., Hilbert H.,
RA	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Delaire V., Mortier S.,
RA	Calbert F., Ayres S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA	Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA	Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,

Jerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.J. THE GENOME SEQUENCE OF SCHIZOSACCHAROMYCES POMBE. *Nature* 415:81-880 (2002).

- - - - - FUNCTION: REGULATES UBIQUITINATION OF CDC25. CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP diphosphate + protein N-ubiquityllysine.

- - - - - MISCELLANEOUS: A cysteine residue is required for ubiquitin thioester formation.

- - - - - SIMILARITY: Contains 1 C2 domain.

- - - - - SIMILARITY: Contains 3 WW domains.

- - - - - SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.

- - - - - SIMILARITY: STRONG, TO YEAST RSP5.

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Nature 387:78-81(1997).  
 [2] IDENTIFICATION.  
 Winston P.; unpublished observations (FEB-1993).  
 CHARACTERIZATION.  
 [3] STRAIN=Sigma 96154-942; PubMed=8596462;  
 Hein C., Springael J.-Y., Volland C., Hagenauer-Tsapis R., Andre B.;  
 MEDLINE=96154-942; PubMed=7705685;  
 "NPR1, an essential yeast gene involved in induced degradation of Gap1  
 and Fur4 permeases, encodes the Rps5 ubiquitin-protein ligase.";  
 Mol. Microbiol. 18:77-87(1995).  
 FUNCTION.  
 MEDLINE=95281634; PubMed=7761480;  
 Huibregtse J.M., Schieffner M., Beaudenon S., Howley P.M.;  
 "A family of proteins structurally and functionally related to the  
 E6-AP ubiquitin-protein ligase.";  
 Proc. Natl. Acad. Sci. U.S.A. 92:2563-2567(1995).  
 [5] PROTEIN DOMAIN.  
 MEDLINE=95281634; PubMed=7761480;  
 Huibregtse J.M., Schieffner M., Beaudenon S., Howley P.M.;  
 Proc. Natl. Acad. Sci. U.S.A. 92:2549-5249(1995).  
 CHARACTERIZATION.  
 MEDLINE=FY56;  
 Wang G., Yang J., Huibregtse J.M.;  
 "Functional domains of the rps5 ubiquitin-protein ligase.";  
 Mol. Cell. Biol. 19:342-352 (1999).  
 -|- FUNCTION: E3 ubiquitin-protein ligase which accepts ubiquitin from  
 an E2 ubiquitin-conjugating enzyme in the form of a thioester and  
 then directly transfers the ubiquitin to targeted substrates.  
 REQUIRED FOR UBIQUITINATION AND THEREFORE DEGRADATION OF SEVERAL  
 CELL SURFACE PROTEINS LIKE GAP1, FUR4, MAL61 AND SITE2. ALSO ACTS  
 ON RBPI.  
 -|- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (Potential).  
 -|- PM: THE UBIQUITINATION APPEARS TO BE THE RESULT OF AN  
 INTRAMOLECULAR TRANSFER OF UBIQUITIN.  
 -|- MISCELLANEOUS: A cysteine residue is required for ubiquitin-  
 thioester formation.  
 -|- SIMILARITY: Contains 1 C2 domain.  
 -|- SIMILARITY: Contains 3 WW domains.  
 -|- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase  
 domain.  
 -|- SIMILARITY: TO YEAST YKL010C.  
 -|- SIMILARITY: TO S. POMBE PUB1.

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~ GO:GO-0000151; C:ubiquitin ligase complex; IDA.  
 ~ GO:GO-10004842; F:ubiquitin-protein ligase activity; IDA.  
 ~ GO:GO-0000151; P:chromatin assembly/disassembly; IMP.  
 ~ SGD:S0000977; RSP5.  
 ~ GO:GO-0006513; P:protein monoubiquitination; IDA.  
 ~ GO:GO-0000109; P:protein polyubiquitination; IDA.  
 ~ InterPro:IPR000008; C2.  
 ~ InterPro:IPR000069; HECT\_domain.  
 ~ InterPro:IPR002349; WW.  
 ~ InterPro:IPR001202; WW\_RSP5\_WWP.  
 ~ Pfam:Pf00168; C2; 1.  
 ~ Pfam:Pf00652; HECT; 1.

DR Pfam; PF00397; WW; 3.  
 DR PRINTS; PRO0403; WW DOMAIN.  
 DR SMART; SMO039; C2; 1.  
 DR SMART; SMO0119; HBCT; 1.  
 DR PROSITE; PS00499; C2 DOMAIN 1;  
 DR PROSITE; PS50004; C2 DOMAIN\_2; 1.  
 DR PROSITE; PS01159; WW DOMAIN 1;  
 DR PROSITE; PS50020; WW DOMAIN\_2; 3.  
 DR Ubi conjugation pathway; Ligase; Repeat.  
 FT DOMAIN 1 88 C2 DOMAIN.  
 FT DOMAIN 229 262 WW 1.  
 FT DOMAIN 315 322 WW 2.  
 FT DOMAIN 331 364 WW 3.  
 FT DOMAIN 387 420 WW 3.  
 FT DOMAIN 705 809 HECT.  
 FT BINDING 777 777 UBIQUITIN.  
 FT VARIANT 733 733 L > S (IN RSP5-1; IMPAIRED IN UBIQUITIN-  
 THIOESTER FORMATION AND CATALYSIS OF  
 SUBSTRATE UBIQUITINATION).  
 FT MUTAGEN 777 C>A; LOSS OF UBIQUITINATION.  
 SQ SEQUENCE 809 AA; 91816 MW; 6P13638447E70P CRC64;  
 Query Match Score 35.5%; Length 809;  
 Best Local Similarity 35.0%; Pred. No. 5; se-32;  
 Matches 313; Conservative 131; Mismatches 238; Indels 164; Gaps 24;

Qy 3 SSIIKIRIYLCAKNLAKKDFPFPIVDPFPKAVTYDGSOCCHSTDTVKNTLDPKMWHYDL-Y 61  
 Db 3 SSISVKL- -VAABSLYRKDVFRSPSDPAVLTDGY-QTKTSAAKTLNPNWNEFKFDD 59

Qy 62 VGTDSITISVNHKKTHKKQGAGF-GCVRL-LSNASRLKD----TGQR----LDI 110  
 Db 60 INENSIHLIQVFFQKKF-KKCDQGFLGVNVYRVGDVIGHLDDETTSSGRPREETITRDL 118

Qy 111 CKLAFSDTDAVRQIVV-----SLQTDRIGTGSVVDGRLL 148  
 Db 119 KKS-N-DGMWSGRLLIVLSKPLSSSPHSQAPSGHTASSSTNTSSSTRNGHSTS--T 173

Qy 149 ENEGTVIBDSSGRPLSFMEDAP-----YTDSTGAAA----- 182

Db 174 RNHSTSHPSRGTAQAVESTLQSQTAAATNTATSHRSTNSPATQYSSFFEDQYGRLLPP 233

Qy 183 -----GGGNCRFVE-----SPSDQDQLAQRLNPFDVGSLOTBONR---PHG 222

Db 234 GWERTDNFGRTYIVDHNTRTTWKRFILDQ\_TEARGNQLNANTELBQRGRTLPGG 292

Qy 223 HQS-----PELPEGYBQRTTVQGQVYFLHT 247

Db 293 SSDNSSVTVQVGGGSNTPPVNGAAAFAATGGTTSGLGEPSGMWQRFTPEGRAYFVDH 352

Qy 248 QTGYSTMIDPRIRDANSV-----CDBLGILPPGMEVRSVTSVSGTIFYFDHNRT 297

Db 353 NTRTTWDPRRCQYIRYGTGPTTICQQPPVSQQLGPSPSGRMELNTARVVFHDNKT 412

Qy 298 TQFTDPRLHHMHQCLKEPSOPLIPSEGSELEDELPQRYERLVQKLKVLRHELSI 357

Db 413 TWDPR-----LPS---SL-DQNP---QYKDFRRKTVYFSQPAL 448

Qy 358 QQPOQHCRIVSREELFEESTSYRQIMKRPDKLKLVMKFRGEGLDYGCVAREMLYL 417

Db 449 -RILPGQCHIKVRRKTFEDAYCEINQTPPELKRIMKEDGEELDYGVSREFFL 507

Qy 418 CHEMINPYGLKPIOLSDLESVPDPLHKSILWVLENDTPVLDHTFCYEHNAFRGLQHELK 477

Db 508 SHENENPYFCLEPLSAYDNYTQINPNQGNGINPHEHLYKEFGRVGLGVFHRFLDAFPV 567

Qy 478 VEFYKQLIKPKIOLSDLESVPDPLHKSILWVLENDTPVLDHTFCYEHNAFRGLQHELK 537

Db 568 GALXKMRJRKVVLQDMEGVDAEVNSLNWMLENSIDGVLLTFSADDERFGEVVTVDLX 627

Qy 538 PNRGNVPVTEENKKEYVRLYNNTRMEGIEAQFLALQKGFNELIPOHLIKEFQKELLI 597

628	PDGRIEVTGDKKEVYLYTQARIIVDRYEQOFKAEMDGENELIPEDLVTFDERBELL	687
598	IGGLDKIDLNWKSTRNLKHCIVADSNIVRMWQAVETDEBERLQLQFTGSTRVPLOG	657
668	IIGSARADIDWKKRTHDYRQIQQESSEDEVIFWKCSWENNEQARLLQFTGTSR.PVNG	747
658	PKALQGSTGAAGAPRLPTHTLIDANTDNLPKAHTCFNRIDIPPEYESKLYEKILATAVEET	717
748	FKDQGSD---GPRTIERA-GEVQQLPKSHTCNVRDLPQYDYSMKQKLTIAVEET	803
718	CQFANE	723
804	IGFQQE	809
MULT 7		
NE04_HUMAN	STANDARD;	PRT;
P4934;		927 AA.
01-NOV-1995	(Rel. 32, Created)	
01-NOV-1995	(Rel. 32, Last sequence update)	
15-SEP-2003	(Rel. 42, Last annotation update)	
NEDD4-4 Protein (BC_6.3.2.-)	(Fragment).	
NEDD4 OR KIAA0093		
Homo sapiens (Human)		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. NCI_TaxID=96001; [1]		
SEQUENCE FROM N.A.		
TISSUE=Dome mouse; PubMed=7788527; MEDLINE=95308325;		
Nagase T., Miyajima N., Tanaka A., Suzuka T., Seki N., Sato S., Tabata S., Ishikawa K.-I., Kawarabayashi Y., Kotani H., Nomura N.; "Prediction of the coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by analysis of cDNA clones from human cell line KG-1.", DNA Res. 2:37-43 (1995).		
-1- FUNCTION: E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM AN E2 UBIQUITIN-CONJUGATING ENZYME IN THE FORM OF A THIOESTER AND THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATES (BY SIMILARITY).		
-1- MISCELLANEOUS: A cysteine residue is required for ubiquitin-thioester formation.		
-1- SIMILARITY: TO NEDD-4 PROTEIN.		
-1- SIMILARITY: Contains 1 C2 domain.		
-1- SIMILARITY: Contains 4 WW domains.		
-1- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.		
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EMBL: D42055; BAA07655; 1; -.		
HSSPC; Q12556; IPIN.		
Geneva; HGNC:7727; NEDD4.		
MIM: 602278; -.		
PRINTS; PF00397; WW; 4.		
PFam; PF00632; HECT; 1.		
PFam; PF00397; WW; 4.		
PRINTS; PR00360; C2DOMAIN.		
InterPro; IPR000008; C2.		
InterPro; IPR000567; HECT domain.		
InterPro; IPR001202; WW_RgsP5_WWP.		
PFam; PF00116; C2_1.		
PFam; PF00632; HECT; 1.		
SMART; SM00239; C2_1.		
SMART; SM00119; HECTC; 1.		
SMART; SM00456; WW; 4.		

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EMBL; D42055; BAA07655; 1; -.  
HSRP; Q13526; 1PIN.  
GeneID; HGENC;7727; NEDD4.  
MIM; 602278; -.  
GenBank; M30008; C2.  
InterPro; IPR000569; HECT domain.  
InterPro; IPR001202; WW\_RBB5\_WNP.  
PFAM; PF00168; C2; 1.  
PFAM; PF00632; HECT; 1.  
PFAM; PF00397; WW; 4.  
PRINTS; PRO02380; C2DOMAIN.  
SMART; SNO0239; C2; 1.  
SMART; SNO0111; HECTC; 1.  
SMART; SNO0456; WW; 4.

587 KPFQKELELIIIGGLKIDLANDWKSNTRLKH-CYADSNIVRWFHQAVETFDEERRABLIQ 645  
 793 KLFDENELIEMCGLGSDVNDWREHTKYNGSYANHQTIQWPFKAVLNMDSSKRIRILQ 852

646 FVTGSTRVPLQCFKALOGSTGAAGPFLTHLIDANTDNLPKAHTCENRIDPPIYESYEK 705  
 853 FVTGSTRVPMGSAELYGSN--GPQSFTEQW-CTPEKLPRANTCENRIDPPIYESSEE 908

706 LWEKLILAVEETCGF 720  
 909 LWDKLQMAIENTQGP 923

**ULT\_8**  
<sub>14</sub> MOUSE STANDARD; PRT; 957 AA.  
 P6935; 01-NOV-1995 (Rel. 32, Created)  
 15-SEP-2003 (Rel. 34, Last sequence update)  
 NEDD-4 protein (EC 6.3.2.-) (F-fragment).  
 Mus musculus (Mouse).  
 Fukuyama; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1] SEQUENCE FROM N. A.  
 TISSUE=mbrain;  
 Kumar S., Tomooka Y., Noda M.;  
 "Identification of a set of genes with developmentally down-regulated  
 expression in the mouse brain.",  
 Biochem. Biophys. Res. Commun. 185:1155-1161(1992).  
 [2] REFERENCES.  
 Kumar S.; (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 -> FUNCTION: E3 ubiquitin-protein ligase which accepts ubiquitin from  
 AN E2 ubiquitin-conjugating enzyme in the form of a thioester and  
 then directly transfers the ubiquitin to targeted substrates (BY  
 SIMILARITY).

-> FUNCTION: INVOLVED IN THE EMBRYONIC DEVELOPMENT AND  
 DIFFERENTIATION OF THE CENTRAL NERVOUS SYSTEM.

-> TISSUE SPECIFICITY: BRAIN.

-> MISCELLANEOUS: A cysteine residue is required for ubiquitin-thioester formation.

-> SIMILARITY: Contains 1 C2 domain.

-> SIMILARITY: Contains 3 WW domains.

-> SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.

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EMBL; D8A1414; BAA12803.1; -.  
 HSSP; Q13526; 1PIN  
 MGD; MGI:3729; Necl4.  
 GO; GO:0005B29; Cytosol; IDA.  
 GO; GO:0000151; Ubiquitin ligase complex; IDA.  
 GO; GO:0005515; Protein binding activity; IDA.  
 InterPro; IPR000008; C2.  
 InterPro; IPR001205; WW\_RSP5\_WWP.  
 Pfam; PF006168; C2; 1; WW\_RSP5\_WWP.  
 Pfam; PF00632; HECT; 1.

DR Pfam; PF00397; WW; 3.  
 SMART; SN00023; C2; 1.  
 DR SMART; SN00456; WW; 3.  
 DR PROSITE; PS00499; C2 DOMAIN 1; 1.  
 DR PROSITE; PS00004; C2 DOMAIN\_2; 1.  
 DR PROSITE; PS05037; HECT; 1.  
 DR PROSITE; PS01159; WW DOMAIN 1; 3.  
 DR PROSITE; PS50020; WW DOMAIN\_2; 3.  
 KW Ub conjugation pathway; Ligase; Repeat.  
 PT NON\_TER 1  
 FT DOMAIN 150 236 C2 DOMAIN.  
 PT DOMAIN 319 352 WW 1.  
 PT DOMAIN 475 508 WW 2.  
 PT DOMAIN 530 563 WW 3.  
 FT DOMAIN 851 957 HECT.  
 FT BINDING 924 109967 MW; 1  
 SQ SEQUENCE 957 AA; 109967 MW; 1  
 UBQUITIN (BY SIMILARITY);  
 Best Local Similarity 31.5%; Score 1225;, DB 1;  
 Matches 291;保守性 33.6%; Pred. No. 7.5e-81;  
 Best Local Similarity 31.5%; Score 1225;, DB 1;  
 Matches 291; Mismatches 123; Indels 214; Gaps 23;  
 Qy 7 IRLTYLCAKNLAKDFRFLDPFKAV---VTDGSGQCHSSTDVTWNLDPKWNQH---- 58  
 Db 150 VRVVIAGIGLAKDILGASDPPVTRVLDPMSGILTSVQTKTISLNPKWNEELLFRV 209  
 59 --- DLYVCKTD-SITISVWN---- 103  
 Db 210 LPQRHRILPEVDENRLPDDFLQVDPVLPPTENPRMERTPKDFVLPHPRSKSRV 269  
 Qy 84 AGFLGGCVRLSNAISRLKD---- 103  
 Db 270 RGYL----RLKATYLPGNSDENDAQAEELEPGVVILQDPAATHLPHPPEP 318  
 Qy 104 ---GY-QRLDLC---- 103  
 Db 319 SPLPPSWEEQQDVIGRTTYVNHEEFTTWRKRPSPDDDTIDEDNDMQLQQAFTTRRQI 378  
 Qy 136 GTGGSVUDRCILIN---- 171  
 Db 379 SEDVGDPDNRESPENWEIVREDENTEVSQAOVSPPSHIDYQTHLAEFFNTRLAVCGNP 438  
 Qy 172 A--PYTDSTGAAAGG--NCRFVTPSPSDQRLQAQRLRNPDVRSLSQTQNPRPHQSP 226  
 Db 439 ATSQPTTSSHSRSQSLQTCTIFEQPLPVLPJT----SS 475  
 Qy 227 ELPEGYEQRTTQGOVYFLQTQSTWDP----RIPDL-NSVNCDELGPUPG 277  
 Db 476 GLPQHBEKDDGRRSYYDHNSKTTSNSKPTQDDPSRSKIAHLRGKTDNSDLGPUPG 535  
 Qy 278 WERVSTVSGRTYFVDHNNRTQFDPRGHIMHQCLQKEPSQPLPSEGSDEDEELPA 337  
 Db 536 WEBRITHDGRVFFHNIKXTQWEDPLRQNV---AITGPAPV---- 574  
 Qy 338 QRYERDLOVKVLRLHELSLQQPQAGHCRIEVSEETIPEESYRQIMKMRPKD-LKCRLMV 396  
 Db 575 -YSRDYKRYEPRKRLKQTDLFNKPKMLRANILEDSTRTMGYKRADLKLRLWI 632  
 Qy 397 KPRGEGLDYGVAEWLYLICHMINPYYGLFOYSTDNIMLQINPQDSSI-NPDHLSYF 455  
 Db 633 ESDGEKOLDYGSVAREWFLISKENFNPYGLFXYSATDNYTQINPNSGLCNEBDHLSYF 692  
 Qy 456 HFVGR;MGLAVFHGHINGFTVPPYKOLGKPQLSDLESDYDPELHSLSVILENDITP 515  
 Db 693 KTGIGYAGMAYHGKULDGFFTRPYKOMLQKLTLHOMEVSSEYSSLWLENDETE 752  
 Qy 516 VDQHTFCVERNAFGRILQHELKPNGRNPVTEENKEYRLYNNWRMFGIEQFLAQK 575  
 Db 753 -LDLRFIDEELRGQTHQELKGTGSSEIVVTTNKKKEYTLYCWRFRNTRQOMAAKE 811  
 Qy 576 GENELIPOHLLKPFDEKELELIIIGGLKIDLDNDSRNTPLKHCVWA-DSNIVRMWQAVBT 634





432 STDNTIYQINDDSINPDHLSYFHVGRINGLAVPHGYTINGGTFVFKQLLGKPIQL 491  
 433 :  
 593 D-ESTKLFWENPSSF---ETEGQFTLIGIVLGLAIVNCIDLVHFMVTVYRKLMKKGTF 648  
 594 SDIEVDPEHLKSSLWIL---ENDITPVLDHTFCPV-BEIAFGRLPKDQKELELIGGLDKI 548  
 595 NICKEYVRYLYNNWRMFRGIEAQFLAQKGF---NEIJPQHLLKPFDPQEELLIQGGLDKI 604  
 596 649 RDIDGSHSPVLYOSKLDLLEYGNEDMMTFOISQTDLFGNPMYDLKENGDKAPITNE 708  
 597 NRKEFVNLYSDILNKSVEQPKAFARRGGHMVTNEESPLKYLFRP--EEIELLICSRNL 765  
 598 605 DLNDWKNTNLK-HCVADSNTYRWFQAVETDEERARLQIQFTGSTRVLOGFALOG 663  
 599 766 DFALEATTIPEGDGGTYRSVSLREFWEVHSFDQEQRLQFQTGTDRAVGGLKJLKM 825  
 600 664 STGAAGPRLTHILDANTDNLPKAHTCFCNRDIPPYSEKLYEKLTAVETCGFAV 722  
 601 826 IIANGP-----DTERLPTSHTECFNVILLEPEYSSKEXLKERILKATYAKGFGM 874

MULT 11

A MOUSE  
 UB3A MOUSE STANDARD; PRT; 885 AA.  
 008759; P97482;  
 30-MAY-2000 (Rel. 39, Created)  
 30-MAY-2000 (Rel. 39, Last sequence update)  
 28-FEB-2003 (Rel. 41, Last annotation update)

Ubiquitin-protein ligase E3A (EC 6.3.2.-) (Oncoogenic protein-associated protein E3A).  
 UBE3A.

Mus musculus (Mouse).  
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI-TaxID=10909;  
 [1]

SEQUENCE FROM N.A.  
 STRAIN=C57BL/6 X CBA;  
 MEDLINE=9732076; PubMed=9182527;  
 Hatakeyama S., Jensen J.P., Weissman A.M.: "Subcellular localization and ubiquitin-conjugating enzyme (E2) interactions of mammalian HECT family ubiquitin protein ligases." J. Biol. Chem. 272:15055-15092 (1997).

[2] SEQUENCE FROM N.A.  
 STRAIN=BALB/c; TISSUE=Brain;  
 MEDLINE=9726343; PubMed=9110176;  
 Succliffe J.S., Jiang Y.-H., Gallaard R.-J., Matsuura T., Fang P., Kubota T., Christian S.L., Bressler J., Cattanach B., Ledbetter D.H., Beaudet A.L.: "The E6-AP ubiquitin-protein ligase (UBE3A) gene is localized within a narrowed Angelman syndrome critical region." ; Genome Res. 7:368-377(1997).  
 -1- FUNCTION: E3 ubiquitin-protein ligase which accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates.  
 -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.  
 -1- TISSUE SPECIFICITY: Most abundant in brain, heart and thymus.  
 -1- MISCELLANEOUS: A cysteine residue is required for ubiquitin-thioester formation.  
 -1- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.  
 -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-38 IS THE INITIATOR.

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RESULT 12

L4	YEAST	STANDARD;	PRT;	892 AA.	Query Match 12.4%; Score 481.5; DB 1; Length 892;
P40365;	(Rel. 31, Created)			No. 5.8-27;	Best Local Similarity 31.7%; Pred. No. 5.8-27;
01-NOV-1995	(Rel. 32, Last sequence update)			Mismatches 77;	Best Matches 128; Conservative 156;
28-NOV-2003	(Rel. 41, Last annotation update)			Indels 43;	Gaps 11;
Probable ubiquitin-protein ligase HUL4	(BC 6.3.2.-)				
HUL4	Probable ubiquitin-protein ligase HUL4 OR J1608				
YJR016C	(Baker's yeast)				
Buxuryocea	Fungi; Ascomycota; Sacccharomyces; Saccharomyces cerevisiae				
Saccharomyces cerevisiae	(Baker's yeast)				
Ascomycota					
Saccharomyces cerevisiae					
Saccharomyces cerevisiae					
[1]					
NCBI_TaxID:4332;					
SEQUENCE FROM N.A.					
STRAIN=S238C;					
MEDLINE=9539795;	Pubmed=7568047;				
Huang M.-E., Chuat J.-C., Galibert F., Swagelmakers S.M.A., van de Putte P., van Gool A.J., Verhaeghe R., Swagelmakers S.M.A., van de Putte P., Browne J., Troelstra C., Bootstra D., Hoijmakers J.H.J., "Analysis of a 42.5-kb DNA sequence of chromosome X reveals three tRNA genes and 14 new open reading frames including a gene most probably belonging to the family of ubiquitin-protein ligases.", Yeast 11:775-781(1995).					
[2]					
SEQUENCE OF 362-892 FROM N.A.					
MEDLINE=904531;	Pubmed=7957102;				
van Gool A.J., Verhaeghe R., Swagelmakers S.M.A., van de Putte P., Browne J., Troelstra C., Bootstra D., Hoijmakers J.H.J., "RA26, the functional S. cerevisiae homolog of the Cockayne syndrome B gene ERCC2.", EMBO J. 13:5361-5369 (1994).					
[3]					
GENE NAME, AND GENE ID					
NAME=GND7972; PubMed=9838556;					
Wang G., Yang J., Huibregtse J.M., "Functional domains of the p53 ubiquitin-protein ligase.", Mol. Cell. Biol. 19:342-352 (1999).					
-!- FUNCTION: PROBABLE E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM AN E2 UBIQUITIN-CONJUGATING ENZYME IN THE FORM OF A THIOESTER AND THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATES. NON ESSENTIAL.					
-!- SUBSTRATE: A CSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-THIOESTER FORMATION (BY SIMILARITY).					
-!- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.					
-----					
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-----					
EMBL; L3544; AAA88738.1; SMART; SM00119; HECT; 1; PROSITE; PS5037; HECT; 1; Ubl conjugation Pathway; Ligase.					
DOMAIN 792 892 HECT. DOMAIN 792 860 UBIQUITIN (BY SIMILARITY).					
BINDING 860 860 UBIQUITIN (BY SIMILARITY).					
CONFLICT 362 362 H -> Q (IN REF. 2).					
CONFLICT 410 410 T -> M (IN REF. 2).					
CONFLICT 418 418 T -> I (IN REF. 2).					
CONFLICT 514 519 ESSRWWADPPFDKSKG -> KKAHVHGLPLTLQILTNQ R (IN REF. 2).					
CONFLICT 607 705 V -> A (IN REF. 2).					
CONFLICT 724 724 KH -> ND (IN REF. 2).					
SEQUENCE 892 AA; 103456 MW; 35EP2A8DDA92BD84 CRC64;					
-----					
CC -I- SIMILARITY: Contains 7 RCL repeats.					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration					



Matches 142; Conservative 94; Mismatches 208; Indels 122; Gaps 24;

CC THIOESTER AND THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED  
CC SUBSTRATES. NON ESSENTIAL.

CC MISCELLANEOUS. A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-

CC -!- THIOESTER FORMATION (BY SIMILARITY).

CC -!- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase

CC domain.

CC ---

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC ---

CC DR EMBL: X99960; CAA68221; 1; -;

CC DR EMBL: Z72663; CAA9853; 1; -;

CC DR PIR: S64155; S64155;

CC SGD: S0003109; YGL141W.

CC DR InterPro: IPR000569; HECT\_domain.

CC DR Pfam: PF0643; HECT; 1;

CC DR PROSITE: PS02027; HECT; 1;

CC DR KWD: Conjugation pathway; Ligase.

CC FT DOMAIN: 810 910 HECT.

CC SQ SEQUENCE: 910 AA; 105565 MW; 6DB832A8A81CD19 CRC64;

CC Query Match Score 354; DB 1; Length 910;

CC Best Local Similarity 23.7%; Pred. No. 1..17;

CC Matches 136; Conservative 93; Mismatches 212; Indels 132; Gaps 20;

CC ---

QY 220 PHGOSPELPEG-----YEQTIVQGVYFLTGTVSTWHDRIPRDLNSYNCDELG 272

Db 395 PKBRNPNLKEAVPLLRVYER----DSRLFLSTNN-----428

QY 273 PLPGCWEVRSTYSGRIVFDHNRRTQFTDRLHHHMN----HQCQLKEPSQPLPSE 327

Db 429 -PTYW-----NSEQFLNTRFEEELQEYEDLVEHLEESDE-DMEKE 470

Qy 328 GSLLDEELPAQ----RYERDLVQKVLVRHLBSLQP-----360

Db 471 IDLDKERPLKSLLNKWRKKSSSLRKLEELLPFFPEERVDSLFLDKKR 530

Qy 361 ---SAGHCRIE-----VSREBIEFEFSYRQIMKRPK-----DLKRLMLMVKF 398

Db 531 LSDDDHLLINNMPWASTGKQKOSAIIISRNLEDAFNAFNSIGERFKASLDTPINEF 590

Qy 399 RGEFGGLDGGVAREWLYLCLHE-MLNPPYYGLFQYSTDNTIYMLQINPDSSINPDLSYFHF 457

Db 591 GEERAGIDGGGITEKFLLTVSDGKDFKPHELLR--TDNYR-EIPLSVVYDATKLKYINF 646

Qy 458 VGRIMGLAVFHGHYINGGFTVBFYKQIL---GKPIQLQSLDESTPELKSLYWILE-N 511

Db 647 LGKVNGKCLYERHTLVIDSFADFLKLUNTYNGFLGSFSDGSGSYOSVLYNLKULNMNT 706

Qy 512 DITFVLDHTPCV-EHNAFGRIQLQHELKPNGRNVPYTHEENKEYVPLVYNNRFMGERIAQF 570

Db 707 DEIKSLDTTEIEBEPESSAKVY-DLIPNGSRTYTKDNVLYTKVTDKLNKRCEKPV 764

Qy 571 LALOKGFNHELIPLPHLKPQKZELIELIGG-LDKDIDNDWSNTTRLKHCVADSNIVRMW 629

Db 765 SAFFGGLSVIIAHMMMFNSTELQMLISGERNDIDDLQKSNTBYGGKEEDQITDVFW 824

Qy 630 QAVTFDEERRALLQFTVGSTRVPLQGFLAQSGTGAAPRLFTHLIDANTD--NLPK 687

Db 825 EVLNNEFKEEKFLKETVSYFOAPIOQGXFLDPKEG-----IRNAGTCKYRLPT 874

Qy 688 AHTCFNRIDIPPEYESYKLYELLTAVETCGF 720

Db 875 ASTCVNLKLPDPNKTILREKLVAINSGRF 907

CC ---

CC SEQUENCE FROM N.A.  
MEDLINE=97197983; PubMed=9046099;  
Voet M., Defor E., Verhaest P., Riles L., Robben J., Volckaert G.;  
"The sequence of a nearly unclonable 22.8 kb segment on the left arm  
chromosome VII from *Saccharomyces cerevisiae* reveals genes ARO2, RPL9A,  
TIP1, MRF1 genes and six new open reading frames.",  
yeast 13:177-182 (1997).  
[2] GEN NAME, AND GENE DISRUPTION.  
MEDLINE=90077972; PubMed=985855;  
Wang G., Yang J., Huibridge J.M.;  
"Functional domains of the r805 ubiquitin-protein ligase.",  
Mol. Cell. Biol. 19:3421-352 (1999).  
-!- FUNCTION: PROBABLE E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS  
UBIQUITIN FROM AN E2 UBIQUITIN-CONjugating ENZYME IN THE FORM OF A

arch completed: February 20, 2004, 15:26:05  
b time : 13.8131 secs

GenCore version 5.1.6  
 Copyright (C) 1993 - 2004 Compugen Ltd.

1 protein - protein search, using sw model

in on: February 20, 2004, 15:25:26 (without alignments)  
 5501.382 Million cell updates/sec

title: US-10-009-945-2

urfect score: 3.84  
 sequence: 1 GGSSIKRILVCAKLNKK.....EKLYEKULTAVEETGFAVE 723

oring table: BloSUM62

Gapop 10.0 , Gapext 0.5

sarched: 830525 seqs, 25805264 residues

total number of hits satisfying chosen parameters: 830525

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Minimum Match 10%

Maximum Match 100%

Listing first 45 summaries

atabase : SPTREMBL 23;\*

1: sp\_archaea;\*

2: sp\_bacteria;\*

3: sp\_fungi;\*

4: sp\_human;\*

5: sp\_invertebrate;\*

6: sp\_mammal;\*

7: sp\_minc;\*

8: sp\_organelle;\*

9: sp\_phage;\*

10: sp\_plant;\*

11: sp\_rodont;\*

12: sp\_virus;\*

13: sp\_vertebrate;\*

14: sp\_unclassified;\*

15: sp\_virus;\*

16: sp\_bacteriopl;\*

17: sp\_archaea;\*

17 1234 31.8  
 18 1228.5 31.6  
 19 1228.5 31.6  
 20 1228.5 31.6  
 21 1228.5 31.6  
 22 1227.5 31.6  
 23 1226 31.6  
 24 1225 31.5  
 25 1225 31.5  
 26 1225 31.5  
 27 1224 31.5  
 28 1223.5 31.5  
 29 1215 31.3  
 30 1214.5 31.3  
 31 1213 31.2  
 32 1210 31.2  
 33 1207.5 31.1  
 34 1200.5 30.9  
 35 1196.5 30.8  
 36 1196.5 30.8  
 37 1195.5 30.8  
 38 1191 30.7  
 39 1189 30.6  
 40 1151 29.6  
 41 1129 29.1  
 42 1047 27.0  
 43 1026.5 26.4  
 44 1002 25.8  
 45 991 25.5  
 46 991 25.5  
 47 988 25.5  
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[6]	SEQUENCE FROM N.A.	QY	Db	427 GNVHSNPANSTPGGGSSRSYTTAATPGQRSSRQQGESSSTRSSRGTRNGTSG 486
"Molecular cloning of a type E3 Ubiquitin ligase.";	"Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases."	QY	Db	428 -----LPSBYEORTTVQQVYFLHTQTGYSWTFEDPRI 259
[7]	SEQUENCE FROM N.A.	QY	Db	487 GGGGGSGQRAYASAIAAANQARPLDLPPEYEMTQQGQVYHTPIPTGYSWTFEDPRI 546
Podos S.-D., Hansen K.K., Wang Y.-C., Ferguson E.L.,	"The Dsmurf ubiquitin-protein ligase restricts BMP signaling spatially and temporally during Drosophila development.",	QY	Db	260 PRDLNS - VNCDELGLPDPGWTRSTVSGRYFDANNRRTQFTDPLAHIM----- 309
"The Dsmurf ubiquitin-protein ligase restricts BMP signaling spatially and temporally during Drosophila development.",	Dev. Cell 1:0-0 (2001).	QY	Db	547 PRDFDTQHLLDAIGPLPSGWWORKTASGRYFDANNRRTQFTDPLSGSLQMMRGT 606
[8]	SEQUENCE FROM N.A.	QY	Db	310 ---NHQCOLKEPQPQLPLPS-----EG 328
Liang Y.-Y., Lin X., Feng X.-H.,	"dSmurf1, a Smad3 ubiquitin E3 ligase, specifically targets dpp-activated Mad protein for degradation.",	QY	Db	607 VPPPSAANAGTAPPATPATPSAAAAPPQATPASNATPTLTTNPHRIPVPLPQG 666
Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	-1- SIMILARITY: CONTAINS 1 C2 DOMAIN.	QY	Db	329 SLEDEELPAQRYERDLYTQLKYLTHELSLQOFGHQRIESREIFFEESYRQINMQCRPK 388
EMBL; AE003802; AAP57824_3; -.	EMBL; AF216521; AAF21125_1; -.	Db	667 LLEBADL-LPKYKRLD\YKLRLRTEIQLMQQSQRHLR\SRNEFEESRLLKMRK 725	
EMBL; AF41651; AAL09691_1; -.	EMBL; AF46451; AAM09646_1; -.	QY	389 DLKRLLMTKFRGEGLGDDYGGVAREWLYLCHEMLNPNPYGLFOYSTDNQYMLQINPDSIN 448	
HSSP; Q13526; 1PNN.	HSSP; Q13526; 1PNN.	Db	726 DXKRLLMTKFRGEGLGDDYGGVAREWLHLSREMLNPQGLFOYSRDPHYTLQINPDSGVN 785	
FlyBase; FBgn002301N.	FlyBase; FBgn002301N; lack.	QY	449 PDIISYFHFVGRMTGLAVFHGYINGFTVPPYKQLLGKPOQSDLESVDPELHKSLWVI 508	
InterPro; IPR000008; C2.	InterPro; IPR000056; HECT_domain.	Db	786 PDIISYFHFVGRMTGLAVFHGYINGFTVPPYKQLLGKPOQSDLESVDPELHKSLWVI 845	
InterPro; IPR002349; WW_domain.	InterPro; IPR001202; WW_Rps5_WWP.	QY	509 LENDITPVLDHITPCVEINAFCRILQHBEKPNPDRNVPTEENKEYVRLYVWHRFURGIEA 568	
Pfam; PF00168; C2; 1.	Pfam; PF00397; WW; 3.	Db	846 LESNISGLTESTSVEINSFGLVWHLKPGASISPTEEENKEYVRLYVWHRFURGIEQ 905	
PRINTS; PRO0403; WW_DOMAIN.	SMART; SM00239; C2; 1.	QY	569 QFLALQKGKPCELLIPSILRPFDERELVIGGISSIDVNDWRNNTTRIKHTCTNETTQLWV 965	
SMART; SM00456; WW; 3.	SMART; SM00456; WW; 3.	Db	906 QFLALQKGKPCELLIPSILRPFDERELVIGGISSIDVNDWRNNTTRIKHTCTNETTQLWV	
PROSITE; PS00004; C2_DOMAIN_1; 1.	PROSITE; PS00049; C2_DOMAIN_1; 1.	QY	629 WQAVETPDEERRARLLQFVTGSTRVPIQKFALQGSTGAAGPRLFTHL-IDANTTNLPK 687	
PROSITE; PS00237; HECT_1; 1.	PROSITE; PS01159; WW_DOMAIN_1; 2.	Db	966 WQVTEYSEMMARLLQFVTGSTRVPIQKFALQGSTGAAGPRLFTHL-TADVTPLNLPK 1024	
PROSITE; PS00202; WW_DOMAIN_2; 3.	Ligase.	QY	688 AHTCNFNRDIPPYBSYERKLYERLTAVETCGFAVE 723	
SEQUENCE 1061 AA; 115675 MW; 6BBCC550F5129163 CRC64;	Query Match Score 2206; DB 5; Length 1061;	Db	1026 AHTCNFNRDIPPYBSYERKLYERLTAVETCGFAVE 1061	
best Local Similarity 43.0%; Pred. No. 1.8e-172; Mismatches 148; Indels 346; Gaps 14;	RESULTS 3	Q8BSC0 ID Q8BSC0 PRELIMINARY; PRT; 355 AA.		
matches 454; Conservative 108; Mismatches 148; Indels 346; Gaps 14;	Q8BSC0 AC Q8BSC0	AC Q8BSC0		
6 KIRLTIVCARNLAKDDEPFLPDPFAKTVVDDSGQCESTDIVYANTIDPKNQHYDLYVGIK 65	DT 01-MAR-2003 (TREMBLrel. 23, Created)			
14 KYRITIVCARNLAKDDEPFLPDPFAKTVVDDSGQCESTDIVYANTIDPKNQHYDLYVGIK 73	DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
66 DSTTISWNHCKTHKCGAGFUGCVRLSNAISRLKTDGTYORLDCLKLNPSDTCAVRGQI 125	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
74 DATTTVNQRCTHK-GSGFGLGVCPNFIQSLXGAGFRLGKSPDDDELVRGQI 131	DE Hypotheoretical HECT domain (Fragment).			
.126 VVSQDQLTDRIGT---GSYVDCRQLENE-----GTYY----- 155	OS Mhs_musculus (Mouse)			
.132 ITSLSLKGPPSENPLAVPGSDVREPSDSEDLSPEGWEERTDNGRVYTYNHATK 191	OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
.156 ----- 155	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
192 STWDRRRQPGVYVGGSSHATSPQRHNTHNGNSGDRQAPAGTRSTCTNLMNNGHRSRD 251	RN [1] NCBI_TaxID=10090;			
156 -----EDSGGRPLSCMEEPAFYDTSGAAAGGNCRFV----- 191	RP SEQUENCE FROM N.A.			
252 SYTASDQRHSTBEILSSVGKNTSPTPVSAT-TTTGKKTSSNSAGG---RTEQRPT 308	RC STRAIN=C57BL/6J; TISSUE=Embryo;			
.192 ---SPGODQRQLQAQRURNDPVRGSLQTPQNVRGHSQSP----- 227	RC MEDLINE=22356682; PubMed=12466651;			
309 NEPATPISSTTSASVRLHND-NHYTPKHQTNHAPPSTPTSGQONYVNGNAQNG 366	RA The FANTOM Consortium,			
228 ----- 227	RA The RIKEN Genome Exploration Research Group Phase I & II Team;			
367 STSGNGSGQAAQPSQASANGWTQEDAATTTSPTSTTSPRHSQSPPTNISPPASVTPSAN 426	RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";			
SQ 355 AA; 41315 MW; 93B19B4C82F86DD1 CRC64;	RT Nature 420:563-573 (2002);			
SEQUENCE Best Local Similarity 99.7%; Score 1895; DB 11; Length 355;	DR BML: AK034736; BAC2813.1; -.			
FT NON TER 1	KW Hypothetical protein.			



294	-----DSNSLIMQSDSGNDLPLFEMERYTDTGRPYFTDHTRTTWDPAWPLVRPNC 346	Qy	554 VRLVYNNRERMERGJEAQFLALQKGFNELLIPQHLLKRPDQKLELLITGGDXIDNDWKSNT 613
261	-----RDLSNVNCDBLGPLPGLPGRWYRSTVSIGRIFTYFDHNRRTTQFTDPRLHMMHQCC 314	Db	122 VRLYXNNRFLRGIEAQFLALQKGFNELIPQHLLKRPDQKLELLITGGDXIDNDWKSNT 181.
347	GSSTVGSLMQSPLSHLGPLPSGWMLTNSARTYFDVNTKTWTDDPRL ----- 397	Qy	614 RLHCVADSNIYVFWQAVETDEERARLLQFTGTSSTRVPLQGRALQSTGAAGPRLF 673
315	LKEPSQPLPSEGSLDEELPAQYERDLYQKLKVLRHESLQQPOAHHCRTEVSREEI 374	Db	182 RLHCTPDSNIVKFWKAVAPEFDEERARLLQFTGSSRFLQGKALQ--GAAGPRLF 238
398	-----PSALDQDP--QYKCDFRKLJYJYFSQPGM-RPLGQCNVKYVDH 441	Qy	674 THIOLIDANTDNLPKAHTCFNRIDIPPIYESYEKLYYKELTAAVEETCGFAVE 723
375	FEESTYQIMKMRPKDQIKRMLMKFGEEGHLDYGGVAREMYLILCHEMLNPYGLFQYSTD 434	Db	239 THIOLIDACTNLNPKAHTCFNRIDIPPIYESYEKLYYKELTAAVEETCGFAVE 288
442	FEDSYABIMRYSAHDLRKRMIRPFGEDGLDYGGSRSREFLISHKMFDPICLFLFYSAV 501		RESULT 7
435	NIYMLQINPDSSENPDHLSYFHYGRIMGLAVFQGHYINGGFTVFPFKQLQKPIQLSDL 494	054971	PRELIMINARY; PRT; 854 AA.
502	DNYTLQINPHSSINEHNLNFVFRGIVGIAFFRFLDAFFVYSLKKLJRKKVSLADM 561	ID	ID 054971;
495	ESVDPDEHLKSLWILENDITPVLDITFCYEHNAAGRILQHELKPNGRNVPTBENKREYY 554	AC	AC 054971;
562	ESTDAEYRSLKWKYLENDITGILDITFSYTEDIFGEVTRTELTINGENIEYTFENKRYY 621	DT	DT 01-JUN-1998 (TREMBLrel. 06, Created)
555	RLYVNNRERMERGIAQFLALQGENFLIPOLHLKFDFQKELLELIGDIDNDWKSNTR 614	DT	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
622	DLVTERTRSVKREVEQQNAFYSGFVFLSPDLVNTPDERELELLIGISDQDVDEWKSHE 681	GN	GN Ubiquitin protein ligase.
615	LRHCVADSNIYVFWQAVETDEERARLLQFTGTSSTRVPLQGRALFT 674	OS	OS Mus musculus (Mouse).
682	YRTYIATDPYKWFETIAGWKNEDRSKLQFATGTSR.LPVNSFRDQSD---GKRFT 738	RN	RN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
675	IHLIDANT-DNLPKAHTCFNRIDIPPIYESYEKLYYKELTAAVEETCGFAVE 723	RP	RP RESULT FROM N.A.
739	IE--RAGTPDOLPVYHTCPNRLDIDYPSPKDTLHEKLISLAVENTVFGNE 786	RC	RC STRAIN=C3H/HeJ; TISSUE=Kidney; PubMed=462242;
		RX	RX MEDLINE=98122574; Pubmed=462242;
		RA	RA Perry W.L., Hustad C.M., Swing D.A., O'Sullivan T.N., Jenkins N.A., Copeland N.G.;
		RA	RA "The itchy locus encodes a novel ubiquitin protein ligase that is disrupted in a18H mice".
		RT	RT Nat. Genet. 18:143-146 (1998).
		RL	RL "The itchy locus encodes a novel ubiquitin protein ligase that is disrupted in a18H mice".
		CC	CC -!!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
626	SEQUENCE FROM N.A.	DR	DR EMBL: AF037454; AAB99764.1; -.
627	Q96DE7 PRELIMINARY; PRT; 288 AA.	DR	DR HSSP; Q1526; LPN.
	Q96DE7; 01-DEC-2001 (TREMBLrel. 19, Created)	DR	DR MGDB: MGJ:1202301; Itch.
	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	DR	DR InterPro; IPR000008; C2.
	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DR	DR InterPro; IPR00565; HECT_domain.
	Similar to E3 ubiquitin ligase SMURF2 (Fragment).	DR	DR InterPro; IPR002349; WW.
	Homo sapiens (Human).	DR	DR InterPro; IPR001202; WW_Rsp5_WWP.
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.	DR	DR Pfam; PF00168; C2_1.
	[1]	DR	DR Pfam; PF00622; HECT_1.
	SEQUENCE FROM N.A.	DR	DR PRINTS; PRO0403; WW_DOMAIN.
	Strausberg R.; Submitted JUN-2001 to the EMBL/GenBank/DBJ databases.	DR	DR SMART; SM00056; WW; 3.
	SEQUENCE FROM N.A.	DR	DR PROSITE; PS00004; C2_DOMAIN_2; 1.
	NON_TER 1 1 33255 MW; FB243B300E6537 CRC64;	DR	DR PROSITE; PS00237; HECT_1.
	SEQUENCE 288 AA; 33255 MW; FB243B300E6537 CRC64;	DR	DR PROSITE; PS01159; WW_DOMAIN_1; 4.
		DR	DR PROSITE; PS00020; WW_DOMAIN_2; 2.
	KW Ligase.	SQ	SQ SEQUENCE 854 AA; 97975 MW; AAB32D7BF0EBB3D8 CRC64;
			Query Match 33.9%; Score 1318; DB 11; Length 854;
			Best Local Similarity 35.4%; Pred. No. 1.9e-99;
			Mismatches 229; Indels 220; Gaps 29;
		Qy	6 KIRLTVCAK-NLAKEDFRLDPFAKIVDGSSGCHSTDTPVNLDPKWNQHDLYYGK 64
		Db	9 QLQITVISAKLKENKONWFG-PSPYVEVTD-GOSKCKTEKCNNTNSPKWKQPTVITP 65
		Qy	65 TDISITISWNRHKRHKQGAGFLGCYRL-----LSNAISRLKDTGYC-----107
		Db	66 TSKLCFRTVWSHOTL--KSDVLLGTAGLDIVETLKSNNMKLBETVNTLQVGDKPEPTM 122
		Qy	108 -!LDLCKLNPSITDVAEQVTS-----LQTRD--RIGTGGS--VVDRCR 145
		Db	123 GDLSVC---LDGLQVEAEEVNTGETSCSESTTNQDDGCRTRDTRVSTNGSEDPVEAAS 178
	62 NELVDPDLHNSLWILENDITGVLDHTPCVERNAYEIQHELKPNGRKSIPVNEENKEY 121		

146 G-----LNEGTVYEDSGPGRPLSCMEEPAVY-----DSTG 179	RT RT "Recognition and ubiquitination of Notch by Itch, a hect-type E3 ubiquitin ligase"; J. Biol. Chem. 275:35734-35737 (2000).
179 GENKANGNNSPSLNSGG--FKPSRPPR-----SREPPPTRRPASVNGSPSTNSDDG 231	RL RN [3]
180 AA-----AGGNCRFVEPSQ-----DQIQAQR 203	RP SEQUENCE FROM N.A.
232 SSTGSLLPPTNTNTSTSEGATSGLIPIITISGSGRPLATVSQAPLPPCWEQY-----287	RX MEDLINE=98122574; PubMed=9462742;
204 LRNPDVYGSI-----OTPQNPRGHQSPELPGYEQRITVQGGVYFLITQTGVYSTWH 255	RA Perry W.L., Hustad C.M., Swing D.A., O'Sullivan T.N., Jenkins N.A., Copeland N.G.;
288 -----DQHGRVYYDVIVERITWDPE-----PLPPGERRVDMGRIYVDFHFRTTWQ 338	RA "The Itchy locus encodes a novel ubiquitin protein ligase that is disrupted in a18H mice." Nat. Genet. 18:143-146 (1998).
256 DPRIP-----RDL-----NSVNCDELQGPPLPPCWEYR 281	RT RP SEQUENCE FROM N.A.
339 RPTLSVRNTEQWQLQRSQLGANOQNQRIFTYGNQDFATPSQNKEKDPLSPPLPPCWEYR 398	RX MEDLINE=20101262; PubMed=11046148;
282 STVSSGRIFYDTHNNNTTQFTDPRILHINNNHQCQLEKPSQPL-----324	RA Waribors G., Matalkova L., Chen F., Plant P., Rotin D., Gish G., Ingham R., Ernberg I., Dawson T., "Patient membrane protein 2A of Epstein-Barr virus binds WW domain B3 protein-ubiquitin ligases that ubiquitinate B-cell tyrosine kinases." Mol. Cell. Biol. 20:8526-8535 (2000).
399 TDNSGRVYFTVNHTNTRITQEDPR-----SGQNLNE-KPLDEGWNRFTVDGIPYFVDH 450	RL RN [5]
325 -----PSEGSLDEELPAQYERDILVQLKVLR--HELSIQOPQASHCRIEVSRE 372	RP SEQUENCE FROM N.A.
451 NRRATYYIDERTGKSLALDNGPQAYVDRDFKAKYQFWRFCQOLAMPQ---HIKLTIVTRK 506	RX MEDLINE=98133405; PubMed=9641693;
373 EIPESYRQOMKMRPEKDLKLKRMVYKPRGEGLDGYVAREWYLQCHEMINPYGIFQYS 432	RA Wood J.D., Yuan J., Margolis R.I., Colomer V., Duan K., Kushi J., Raminsky Z., Kleiderlein J.J., Sharp A.H., Ross C.A., "Atrophin-1, the DRPA1 gene product, interacts with two families of WW domain-containing proteins." Mol. Cell. Neurosci. 11:149-160 (1998).
507 TLPEFSQQMFSFSQDLRRLWTFPGEGLDGYTAEWNFLSHENLNPMYCFFEYA 566	RN [6]
433 TDNIMLQINPDSSINPDHSYFHVGRIMLAVFHGYINGGFTVYKOLGKPIOLS 492	RP SEQUENCE FROM N.A.
567 GKDNCLQINPASYTINPDHLKYFRIGRFIAMALFHGKFIDTGFSLFYKRLNKVEGLK 626	RX MEDLINE=21218930; PubMed=11318614;
493 DLESTDPELKSLWTLENDITPV-LDTFCYBNAFAFRILQHEDLNGVTPYBTEENKK 551	RA Chen X., Wen S.C., Fukuda M.N., Gavva N.R., Hsu D.W., Akama T.C., "Human ITCH is a Co-Regulator of the Hematopoietic Transcription Factor NF-E2." Genomics 73:238-241(2001).
627 DLESIDPEFVNSLWVKENNIEEGGELFYSVKEIIGEIKSHDLKENGGNILVTEENKE 686	CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
552 EYVRILYVVKFMRGIEAQFIALQKGNFELIPQHLLKPDQKELELIGLDKIDNDWKS 611	DR AB056613; BAB19389-1; -.
687 EYIRVAEFLRSRGTEQQAFFGIFNELLPCQOYQEDAKELEVILGMBDIDNQW 746	DR AF095745; AAK29399-1; -.
612 NTRLKHCVADSNIVWPNQAVETDEERARLQFVTGSTRVPLQGKALGSTGAAGPR 671	DR HSSP; Q13526; 1PIN.
747 HAIYRHYTRTSKQIMFWNQEVKEIDNECRMRLQFVTCRUPVGCFADLMGSN--GPQ 803	DR InterPro; IPR000569; HECT_domain.
672 LPTIHJIDANTDNLKAHCFNRIDIPPESTERYLWELLTAVEETCGFAE 723	DR InterPro; IPR002349; WW_domain.
804 KPCIEKVY-GKENWLFRSHCENRDLPPYKSYEQLKFAIEETEGFGQE 854	DR InterPro; IPR001202; WW_RSP5_WWP.
SULT 8 BY75 PRELIMINARY: PR7; 862 AA.	DR Pfam; PF000168; C2.1.
QBY75 PRELIMINARY: PR7; 862 AA.	DR Pfam; PF00632; HECT; 1.
01-JUN-2001 (REMBLrel. 17, Created)	DR PRINTS; PRO0403; WW_DOMAIN.
01-MAR-2001 (REMBLrel. 17, Last sequence update)	DR START; SM00339; C2; 1.
01-MAR-2003 (REMBLrel. 23, Last annotation update)	DR START; SM00111; HECTC; 1.
Ubiquitin protein ligase Itch.	DR SM0056; WW; 4.
ITCH. Homo sapiens (Human). Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominoidea; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominoidea. NCBI_TaxID=9606; SEQUENCE FROM N.A.	DR PROSITE; PS00004; C2_DOMAIN_2; 1.
01-JUN-2001 (REMBLrel. 17, Last sequence update)	DR PROSITE; PS00237; HECT; 1.
01-MAR-2003 (REMBLrel. 23, Last annotation update)	DR PROSITE; PS01159; WW_DOMAIN_1; 4.
Ubiquitin protein ligase Itch.	DR PROSITE; PS00020; WW_DOMAIN_2; 2.
QY 6 KIRIVLCAK-NIAKKDEFERLPDPFAKIVDGCVRLISNAISRLKDT-----GYQR-----I	KW Ligase. SEQUENCE 862 AA; 98675 MW; A3D960ET7F4DBFFD3 CRC64;
Db 19 QLIDIVTVAKRNENKECNWFG-PSPVTEVTD-----RDKSKTBKCNNTNSPKWKQPLTVVTP 75	Best Local Similarity 34.7%; Pred. No. 4.8e-98; Matches 308; Conservative 126; Mismatches 241; Indels 212; Gaps 26;
QY 65 TDGTTISWNHKKHHKK--QGAGFLGCVRLISNAISRLKDT-----GYQR-----I	Db 76 VSGLHFVWSQTLKSDVLTGALDIYETLKSNMVKLBVVVTLQLGCDKEPTETIGDL 135
MEDLINE=20549573; PubMed=10940313;	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
Qiu L., Joazeiro C., Fang N., Wang H.Y., Elly C., Altman Y., Fang D., Hunter T., Liu Y.C.;	QY 109 DLCKLNPSDTDAVRGQILVSLQT-----RDRTGTGS-----VVDC 144
SEQUENCE FROM N.A.	Db 136 SIC----LDGLQLESEVVTNGETCTCESASQNDGSRSKDETRYSTNGSDDPEDIAGEN 191



640	RARLQEVGTGSTRVPIQGEFKALGGSTGAAGSPRLFTIHLIDANTDNLPKAHTGCFNRDIPP	699		
824	RNBLQEVITGCRPLPGFADLGN--GPQKFCIERY-GRENWLPRSHTCFNRLLDPP	879		
700	YESYKELYKLLTAYBETCGFAVE	723		
880	YSYEQUKERKLLFAFETEGFQE	903		
'SULT 10 IN5A7	PRELIMINARY;	PRT:	911 AA.	
QBN5A7;				
01-OCT-2002	(TrEMBLrel. 22, Created)			
01-OCT-2002	(TrEMBLrel. 22, Last sequence update)			
01-MAR-2003	(TrEMBLrel. 23, Last annotation update)			
	Simulated to neural cell expressed, developmentally down-regulated 4-like.			
Homo sapiens (Human); Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
[1]_TAXID:9606;				
SEQUENCE FROM N.A.				
Straubnberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. - SIMILARITY: CONTAINS 1 C2 DOMAIN. EMBL: BC032597; AAH22597.1; -.				
InterPro: IPR000008; C2.				
InterPro: IPR000569; HECT_domain.				
InterPro: IPR02349; WW.				
InterPro: IPR001202; WW_RPS5_WWP.				
PFam: PF00168; C2_1.				
PFam: PF00532; HECT_1.				
PRINTS: PF00097; WW_3.				
PRINTS: PRO03_60; C2DOMAIN.				
PRINTS: PRO04_03; WWDOMAIN.				
SMART: SM00239; C2_1.				
SMART: SM00119; HECTC_1.				
PROSITE: PS00499; C2_DOMAIN_1; 1.				
PROSITE: PS00004; C2_DOMAIN_2; 1.				
PROSITE: PS00159; WW_DOMAIN_1; 1.				
PROSITE: PS00020; WW_DOMAIN_2; 1.				
SEQUENCE 911 AA; 104921 MW; CB04AAED677A506 CRC64;				
Query Match Score 1269; DB 4; Length 911;				
Best Local Similarity 33.4%; Pred. No. 2.3e-95;				
Matches 310; Conservative 125; Mismatches 246; Gaps 24;				
2 GSSIKIRLTLVCAKONLAKKDFRLLPEAKI--VVDGSGQCH-STPTVQNLDPKRNQ 56				
17 GBRIRLKVKVSGIDAKKFQDFGSPYVVLISLYADENRELAVQTETKTLNPXWNE 76				
57 HYDLYVKGTD-SITISYWNHKKIHKKQGAGFLGCYRLLSNAI-----97				
77 EPTFRVNPNSNHRLLEFDENRLTDD---FLGQDVPLSLHPLPDMERPYTFDFLL 133				
98 -----SELKDGTGYQRDLICKLNPSDTDAVRQTVLSLQRDRIGTGSVVDORG---- 146				
134 RPRSKSRVK--GFLLKMAATMPKNG----QDEBENSORDMHEGMREVDSNDASQH 186				
147 -----LLENETVY-----155				
187 QEIIPPPPPLPGMEKVDNLGRRTYVHNHNRTTQWHRPSLMDSSESDNNIROINQZAAH 246				
156 -----EDSGP-----GRPLSCFMEEPAAPYTDSTGAA-----AGGGCNCRVES 192				
247 RRRRSRKHSIDELEPESEGDDVPEWETSEEVIAQDSLGLAPPBPASGRSPSQE 306				
193 PSQD-----QRLQAQLRN-----206				

307	LSPLSLRRIQITPDNSGEQFSSLIQREPSSRLCSVTDAVAEQCHLPLAEDGASGSAT	366	Db	
207	-----PDVR-----	226	Qy	
367	NSNHLHLLPQIRPRLSSPPTTSLAPLEGAKDSPVRAVKDTLNPQSFQPSNPSRP	426	Db	
227	B-----LPEGYQORTTVOGQVFHTOTGVSTWHDPPIP-----RDLNNSVNCDELGPL	274	Qy	
427	QHVTQSFUFGBEMTRAPNGPFFDHTNTXITWDPRQLN-----	486	Db	
275	PPGMEYRSTVSQFRIYQFVHDHNETTOFDPRLLHHMNHQCLKEPSQQLPSEGSSLDEBE	334	Qy	
487	PPGWEERTHLDGATFYIDHNSXKITQWEDPRQLN-----	524	Db	
335	LPQORYERDVLQVCKLVRLHESLQQPOAQRHIEVSREEFEESYRQIKM-RPKDILKR	393	Qy	
525	-PAVPSREFKQDYFRKLKRPADIPNRFEMKLHRNNFEESYRQNSVKEPDLVLR	583	Db	
394	LMTKFRGREGGLDGQVAREMLYLCHMLNPYYGQFQYSDDNLYLQINPDSSI-NPDHL	452	Qy	
584	LWTEFSEKGLDGGVAREMLYLCHMLNPYYGQFQYSDDNLYLQINPNSGLCNEDHL	643	Db	
453	SYFIEVGRIMLAFPHGSHYINGGFTVBFYKOLLGAPIQLSDLEYSDPBLHKSLYWILEND	512	Qy	
644	SYFTFIGVAGLAVFGRGKLLDFPFRFYKMLGKQITLNDMESYDSEYNSLWILEND	703	Db	
513	ITPYLDHFTCVENAFARTLQELKNGRNPVTEENKCEYVRLVNVFMRGIEBAQFLA	572	Qy	
704	PTE-LDLMFCIDENFGTYQVDLKGNSEMIVNENKREVDLQWFRVNRVQKQDNA	762	Db	
573	LQKGFNBELIPOHLLPKPQKELELLIGGLDKIDLNWKSNTRLKHCVADSN-TYRWFWQA	631	Qy	
763	FLEETTELLPIDDLIKPDENEELLLMGLGDVDVNDWRSQSIYNGCYCPHPVQFWQA	822	Db	
632	VETDEEERRARLILQVFTGSTRVPLQGFKAQLOGSTGAAGPRLFTIHLIDANTDNPKAHTC	691	Qy	
823	VLMANDAEKIRLQVFTGSTRVPMNGFAELYGSN--GPOLFTFQW-GSPERLUPRAHTC	878	Db	
692	FNRDIPPESTFKLVEYLTAVEETCGF	720	Qy	
879	FNTRDLPPESTFETFEDLREKLMAVENAQGF	907	Db	
RESULT 11				
Q96PUS	PRELIMINARY;		PRT;	955 AA.
ID	Q96PUS			
AC				
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	NEUD3-1 like ubiquitin ligase 3.			
GN	NED3.			
OS	Homosapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	CX			
RN	SEQUENCE FROM N.A.			
RN	SEQUENCE FROM N.A.			
RA	Okanoto Y., Miyazaki K., Sakamoto M., Kato C., Nakagawa A.;			
RA	"Homo sapiens NEUD3-1 like ubiquitin ligase 3."			
RT	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.			
RL				
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=J1269131; PubMed=112441092;			
RA	Harvey F.K., Dinudom A., Cook J.D., Kumar S.;			
RT	"The Nedd4-1 like protein KIAA0439 is a potential regulator of the epithelial sodium channel."			
RL	J. Biol. Chem. 276:8537-8561(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=J1269131; PubMed=112441092;			
RT	Harvey F.K., Dinudom A., Cook J.D., Kumar S.;			
RT	"The Nedd4-1 like protein KIAA0439 is a potential regulator of the epithelial sodium channel."			
RL	J. Biol. Chem. 276:8537-8561(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=J1269131; PubMed=112441092;			
RT	Harvey F.K., Dinudom A., Cook J.D., Kumar S.;			
RT	"The Nedd4-1 like protein KIAA0439 is a potential regulator of the epithelial sodium channel."			
RL	J. Biol. Chem. 276:8537-8561(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=J1269131; PubMed=112441092;			
RT	Harvey F.K., Dinudom A., Cook J.D., Kumar S.;			
RT	"The Nedd4-1 like protein KIAA0439 is a potential regulator of the epithelial sodium channel."			
RL	J. Biol. Chem. 276:8537-8561(2001).			
RN	[3]			

A	F	Ingham R., Ernberg I., Pawson T.; Epstein-Barr virus binds WW domain B3 protein-ubiquitin ligases that ubiquitinate B-cell tyrosine kinases. ";	Qy	410 AREWLYLLCHEMLNPYGLPQYSTDNIMQINPDSSTI-NPDHLSYFHVGRRIMGLAVPH 468
L	M.	Protein: Cell. Biol. 20:8526-8535 (2000).	Db	644 AREWFLLSKEMENPYGLPQYSTDNIMQINPDSSTI-NPDHLSYFHVGRRIMGLAVPH 703
D	-1.	SIMILARITY: CONTAINS 1 C2 DOMAIN.	Qy	469 GHYINGGFTVPPFYQLLGPKIQSDLSVDPHEKSLVWILENDITPVLDHTFCVBHNAF 528
R	InterPro; IPR000008; C2; 1.	InterPro; IPR000049; HECT_domain.	Db	704 GKLQDGFTRPFYKMLGQITLNDMESVDSTYNSKLWILENDPTE-LDLMFCIDEEF 762
R	InterPro; IPR000249; WW; WW_RSPS_WWP.	InterPro; IPR001202; WW_RSPS_WWP.	Qy	529 GRILQHELXENGTRGVPPVTEBNKEKEYVRLYVANWFMRGIEAQFLAQKGFNELIPCHLKP 588
R	Pfam; PF000622; HECT; 1.	Pfam; PF000622; HECT; 1.	Db	763 GQTQYQDLRNGSEMVNTNEKEYIDLIVQNRFPVNQKQMAPLEGFTELLPIDLIKI 822
R	Pfam; PF00339; WW; 4.	Pfam; PF00339; WW; 4.	Qy	589 FDQEKELETLIGGLKIDUDWKSTNLKHCVADS-TYRVFWHQAVETDEERARUQFV 647
R	PRINTS; PRO00403; WWDOMAIN.	PRINTS; PRO00403; WWDOMAIN.	Db	823 FDENEJELINCGLGDVWDWRHSIYNGCNCNNHPVQWFKAVLMDAEKRIRLQFV 882
R	SN2RT; SM00339; C2; 1.	SN2RT; SM00339; C2; 1.	Qy	648 TGSYRVLQGFKALOGSTGAAGGPRLFTHIDANTDNLPKAHTCENRIDIPPYESEKLY 707
R	SN2RT; SM00056; WW; 4.	PROSITE; PS00499; C2_DOMAIN_1; 1.	Db	883 TGTSRVPMMGFAELYGSN--GSQLFTBQW-GSPKLUPLRATCFNRLDLPYETPDLR 938
R	PROSITE; PS00499; C2_DOMAIN_1; 1.	PROSITE; PS00159; WW_DOMAIN_1; 4.	Qy	708 EKLLDAVEETCGF 720
R	PROSITE; PS00159; WW_DOMAIN_1; 4.	PROSITE; PS00202; WW_DOMAIN_2; 1.	Db	939 EKLLMAVENAQGP 951
R	Liase.	SEQUENCE 955 AA; 110021 MW; A8BB278A37FF6A6B5 CRC64;		
		Query Match 32.1%; Score 1247; DB 4; Length 955;		RESULT 12
		Best Local Similarity 31.9%; Pred. No. 1.6e-93;		Q9H451 PRELIMINARY; PPT; 703 AA.
		Matches 310; Conservative 125; Mismatches 246; Indels 292; Gaps 24;		ID Q9H451; AC Q9H451;
		/ 2 GSSKIIRITVCLAKNLAKKDFPFLPFKAKI---VVDGSGQCH --STDYVKTLDPKRNQ 56		DT 01-MAR-2001 (TREMBL: 16; Created)
		) 17 GBFRILRKVKVSGIDLAKKDIFGASDDPVKUSLYADENRELAVALQTKTITKLNPWNK 76		DT 01-OCT-2001 (TREMBL: 18; Last sequence update)
		) 57 HYDLYVYKTD-SITISYWNHKKIHKKQGAGFLGCVYLLSNAI----- 97		DT 01-JUN-2002 (TREMBL: 21; Last annotation update)
		) 77 EFPYRNPNSNHLLFEYFDEERLRLDD--FLGQDVPLSHLPTDPTMERYPTFKDFLL 133		DE D46001.1 (Atrophin 1 interacting protein 4 (AIP4)) (Fragment).
		) 98 -----SRIKDGTYQRLDCKLNKPSTDAYRGQIVTSLQTRDRIGTGGSYVDPRG---- 146		DN DE46001.1
		) 134 RPRSHKSRVK-GFLRLKMAKPNG----QDDBENSQRDNDHEGNEVDSNDASQH 186		OS OS Homo sapiens (Human).
		) 147 -----LLENEGTVY----- 155		OC OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Hominidae; Homo.
		) 187 QSLRPPPPLPPGWEKYDNLGRTRYTNHNNTTQWERSLMDVSSESNDNIRQINQEAH 246		OX NCBI_TaxID=9606; RN [1]
		) 156 -----EDSGP-----GRPLSCFMEEPAAPYPTDSTGAA----AGGGNCRFEVES 192		RP SEQUENCE FROM N.A.
		) 247 RRRPRRHISEDLEPEBSEGDPVPEWETISEVNIAGDSLGLALPPPASPSSRTSFQ 306		RA RA Smith M.; RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
		) 193 PSOD-----ORLQAQRLRN----- 206		DR DR EMBL; ALI09232; CAC09387.2; -.
		) 307 LSELRSRLQIPDNGBFQSSLRQEPSSRLRSCTSVDAAEQQHLPPPSVAYVHTPG 366		DR DR HSSP; Q13526; 1PIN.
		) 207 -----PDVR---- 210		DR DR InterPro; IPR00567; HECT_domain.
		) 367 LPSSGEWERKDAKGRTYYVNENNRTTWTRPIMQLAEDGASGSATNSNNHIEQIRRRS 426		DR DR InterPro; IPR002349; WW.
		) 211 -----GSLQTPNRPHQHSPE-----LPBGEQZR 235		DR DR InterPro; IPR001202; WW_RBD5_WWP.
		) 427 LSSPTVTLSAPLEGAKDSPVRRAVKDTLSNPQSPSPYNSPKHQKVTQSPFLPPGNWMR 486		DR DR Prosite; PS50037; HECT; 1.
		) 236 RTVQGQVYFLHTQGSTWHDRP----RDLNSSVNCDELGPPLPGWVRSTVSGRTYF 290		DR DR Prosite; PS01159; WW_DOMAIN_1; 4.
		) 487 IAPNGRPPFDINTKTTWEDPRKPVHNSKTSISNPNGLPQPGWEERIHDGRTFY 546		DR DR Prosite; PS50020; WW_DOMAIN_2; 2.
		) 291 VDHNNRITQFTDERLHHIMNHOCQLEKPSQPLPLPSEGSLDEELPAQYERDLVQKLKV 350		FT FT NON_TER 1
		) 547 IDRNSKITQWEDRQLN-----PAITG-----PAPVYSRFKQKRYD 583		SQ SQ SEQUENCE 703 AA; 81104 MW; B021DE172A9F1449 CRC64;
		) 220 PHGHSPELPEGFBORTIVQGQYFLHTQTGVSFTWHDPRIP----- 260		Query Match 32.1%; Score 1245.4; DB 4; Length 703;
		) 73 SPATSESDSSTSGLPPNTNTSEATSGLIPI----- 18;		Best Local Similarity 39.8%; Prd. No. 1.3e-93; Matches 274; Conservative 99; Mismatches 180; Indels 135; Gaps 18;
		) 168 MEEPAPYPTDSTGAAAGGCNCRFTESPQDQLRNLNEGTYYEDSGPGRPLSCF 167		Qy Qy 114 NPSPDIDAVRGQIVYSL-----QTRDRIG-TGSSVVDCRGLLENEGTYYEDSGPGRPLSCF 167
		) 73 SPATSESDSSTSGLPPNTNTSEATSGLIPI----- 18;		Db Db 73 SPATSESDSSTSGLPPNTNTSEATSGLIPI-----HISGGGP-RPLNPPV 123
		) 124 TQAPLP-----PGWGRV----- 18;		Qy Qy 168 MEEPAPYPTDSTGAAAGGCNCRFTESPQDQLRNLNEGTYYEDSGPGRPLSCF 167
		) 584 PRKLKKPKDAPINPRFENLHRNNFEESEKGDYGV 643		Db Db 124 TQAPLP-----PGWGRV-----DOHGRYYVDHEKRITWDR 156



Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

-i SIMILARITY: CONTAINS 1 C2 DOMAIN.

EMBL: ALI3746; CAB70754; 1; -.

HSSP: Q15252; 1PIN.

InterPro: IPR000008; C2.

InterPro: IPR00569; HECT\_domain.

Intertier: IPR002349; WW.

InterPro: IPR001202; WW\_RSPS\_WWP.

Pfam: PF00168; C2; 1.

Pfam: PF00632; HECT; 1.

PRINTS: PRO0043; WWDOMAIN.

SMART: SM00239; C2; 1.

SMART: SM00456; WW; 3.

PROSITE: PS50004; C2\_DOMAIN\_2; 1.

PROSITE: PS50337; HECT; 1.

PROSITE: PS01159; WW\_DOMAIN\_1; 3.

PROSITE: PS50020; WW\_DOMAIN\_2; 3.

Hypothetical protein.

NON\_TER 1

SEQUENCE 820 AA; 95233 MW; 0FDB34B29B5F4123 CRC64;

Query Match 32.0%; Score 1241.5; DB 4; Length 820;

Best Local Similarity 34.9%; Pred. No. 3 5e-93;

Matches 294; Conservative 116; Mismatches 230; Gaps 21;

98 -----SRLKDTGYWORLDLCKLNPSDSDAVRGQIVVSIQTRDRIGT 137

69 PTMTERYTFKDFLLRPRSHSRVK-GFRLKHYAMPNG----GDEENSQRDDMEH 121

138 GGSVYDRCG-----LNEGTVY----- 155

122 GWEVVDNSDASQHQEEQLPPPPLPPGWEWKDVNIGRTYVHNHNRTQWHRESLMDVSSE 181

156 -----EDSGP-----GRPLSAPMEEPAFYDSTA-- 181

182 SDNNITIQINOAHHRRRSRRRHISDLEPEPSEG3DVPWPETISEVNIAGSDLSIALP 241

182 --AGGGNCRVEPSQD-----ORLQQRARN----- 206

242 PPPASPOSRTSQESEBSRRIQLTPDNSGEQSIIQREPPSRLCSVTDAEAQGH 301

207 -----PVYRGSLQTPONPFRHQHOSPE-----LPEGYEQRTTYQGGQVYFL 245

302 LPGAKDSDPVRRAVKTLSNQSPQSPNSPKHQKTTQSFLPQGMNR1APNGRPFPI 361

246 HTOQGVSTWDHPRIP----RDLNRYNCDELGPLPQGMNEVRSTYSGRILYFVDHHNNRTQF 300

362 DINTKTTWEDPLRKPVHNRSKTSINPNPLGPQGMERIHDGRTFYIDENSKTQW 421

301 TDPRLHHMHQQCOKKEPSQBLPLPSEGSELEDEELPAQEYERDLVQKLKVRLHELIQQP 360

422 EDPRLQN-----PAITG-----PAVYSREFKQCYDFFRKLCKKPAD 458

361 QAGHCRLEVSREEEFEESEYRQIMKA-RPKDLKELMVKPRGBCLDVGWAREWLJLCH 419

459 IPNRFEMLHENNIFEESEYRIMSKTPRDVLKARWIESESEKGLDYCGVARENEWFLSK 518

420 EMLNPTYGLQFQYSTDNLYMQINPSSI-NPDHISYFHVGRMLGAVFHGHYINGGFTV 478

519 EMFNPYGLFPEYSATNTYLOPNSGLCNEHDHSYFTFGRVAGLAVFHGKLDGFIR 578

479 PFKQKMLGKPIOSLDESDVDELKSLWILNDTPVLDHTCFVHNAGFRILQHBLKP 538

579 PFKXAMMGLKQITLNDMSDSEYYNSLKWILEDE-LDLMCIDEENFGQTYQVDLKP 637

598 NGRNVPTEENKEYVRLYNNWRMGERIAQFLAQKGFNELLQPHLLKPFDCOKELBLII 598

599 NGSEIMVTNENKREYIDLVIQWRFVNRYQKOMNAFLGEGTELLPIDLIKIFDENELLM 697

600 QGKDKIDLNDWSNTPLKHCADSN-IVRKFQAVETDEERARILAFVTSRVPLQG 657

601 CGIGDVFNDNDRQHSIYKNGCPCNHPVQCNKAVLMDAERTRILQFVTCRSVPANG 757

602 FKLQGSTGAAPRLPTHLIDANTDNLPAHTCENRIPPEYESBKLYEKLITAVEBT 717

603 758 PAFLYGN--GPQLETFIQM-GSFPEKLPAHTCENRIPPEYTEDIREKLMAYENA 813

604 PRT; PS5020; WW; 3.

605 PRINTER; IPR001202; WW\_RSPS\_WWP.

606 PRINTS; PRO0043; WWDOMAIN.

607 SMART; SM00239; C2; 1.

608 SMART; SM00456; WW; 4.

609 PROSITE; PS50040; C2\_DOMAIN\_2; 1.

610 PROSITE; PS50237; HECT; 1.

611 PROSITE; PS50159; WW\_DOMAIN\_1; 4.

612 PROSITE; PS5020; WW\_DOMAIN\_2; 2.

613 KW Hypothetical protein.

614 SEQUENCE 922 AA; 105201 MW;

615 SMART; SM00119; HECT; 1.

616 PROSITE; PS50168; C2; 1.

617 PROSITE; PS50365; AAK94668; 1.

618 PROSITE; BC036065; AAH36665; 1.

619 RPRINTS; PRO0443; WWDOMAIN.

620 RPRINTS; PRO0397; WW; 4.

621 RPRINTS; PRO00008; C2.

622 InterPro; IPR002249; HECT domain.

623 InterPro; IPR001202; WW\_RSPS\_WWP.

624 RPRINTS; PRO00237; HECT; 1.

625 RPRINTS; PRO00362; HECT; 1.

626 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

627 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

628 RPRINTS; PRO00237; HECT; 1.

629 RPRINTS; PRO00365; AAK94668; 1.

630 RPRINTS; PRO00168; C2; 1.

631 RPRINTS; PRO00237; HECT; 1.

632 RPRINTS; PRO00365; AAK94668; 1.

633 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

634 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

635 RPRINTS; PRO00237; HECT; 1.

636 RPRINTS; PRO00365; AAK94668; 1.

637 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

638 RPRINTS; PRO00237; HECT; 1.

639 RPRINTS; PRO00365; AAK94668; 1.

640 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

641 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

642 RPRINTS; PRO00237; HECT; 1.

643 RPRINTS; PRO00365; AAK94668; 1.

644 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

645 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

646 RPRINTS; PRO00237; HECT; 1.

647 RPRINTS; PRO00365; AAK94668; 1.

648 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

649 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

650 RPRINTS; PRO00237; HECT; 1.

651 RPRINTS; PRO00365; AAK94668; 1.

652 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

653 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

654 RPRINTS; PRO00237; HECT; 1.

655 RPRINTS; PRO00365; AAK94668; 1.

656 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

657 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

658 RPRINTS; PRO00237; HECT; 1.

659 RPRINTS; PRO00365; AAK94668; 1.

660 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

661 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

662 RPRINTS; PRO00237; HECT; 1.

663 RPRINTS; PRO00365; AAK94668; 1.

664 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

665 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

666 RPRINTS; PRO00237; HECT; 1.

667 RPRINTS; PRO00365; AAK94668; 1.

668 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

669 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

670 RPRINTS; PRO00237; HECT; 1.

671 RPRINTS; PRO00365; AAK94668; 1.

672 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

673 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

674 RPRINTS; PRO00237; HECT; 1.

675 RPRINTS; PRO00365; AAK94668; 1.

676 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

677 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

678 RPRINTS; PRO00237; HECT; 1.

679 RPRINTS; PRO00365; AAK94668; 1.

680 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

681 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

682 RPRINTS; PRO00237; HECT; 1.

683 RPRINTS; PRO00365; AAK94668; 1.

684 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

685 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

686 RPRINTS; PRO00237; HECT; 1.

687 RPRINTS; PRO00365; AAK94668; 1.

688 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

689 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

690 RPRINTS; PRO00237; HECT; 1.

691 RPRINTS; PRO00365; AAK94668; 1.

692 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

693 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

694 RPRINTS; PRO00237; HECT; 1.

695 RPRINTS; PRO00365; AAK94668; 1.

696 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

697 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

698 RPRINTS; PRO00237; HECT; 1.

699 RPRINTS; PRO00365; AAK94668; 1.

700 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

701 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

702 RPRINTS; PRO00237; HECT; 1.

703 RPRINTS; PRO00365; AAK94668; 1.

704 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

705 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

706 RPRINTS; PRO00237; HECT; 1.

707 RPRINTS; PRO00365; AAK94668; 1.

708 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

709 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

710 RPRINTS; PRO00237; HECT; 1.

711 RPRINTS; PRO00365; AAK94668; 1.

712 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

713 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

714 RPRINTS; PRO00237; HECT; 1.

715 RPRINTS; PRO00365; AAK94668; 1.

716 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

717 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

718 RPRINTS; PRO00237; HECT; 1.

719 RPRINTS; PRO00365; AAK94668; 1.

720 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

721 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

722 RPRINTS; PRO00237; HECT; 1.

723 RPRINTS; PRO00365; AAK94668; 1.

724 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

725 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

726 RPRINTS; PRO00237; HECT; 1.

727 RPRINTS; PRO00365; AAK94668; 1.

728 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

729 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

730 RPRINTS; PRO00237; HECT; 1.

731 RPRINTS; PRO00365; AAK94668; 1.

732 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

733 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

734 RPRINTS; PRO00237; HECT; 1.

735 RPRINTS; PRO00365; AAK94668; 1.

736 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

737 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

738 RPRINTS; PRO00237; HECT; 1.

739 RPRINTS; PRO00365; AAK94668; 1.

740 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

741 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

742 RPRINTS; PRO00237; HECT; 1.

743 RPRINTS; PRO00365; AAK94668; 1.

744 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

745 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

746 RPRINTS; PRO00237; HECT; 1.

747 RPRINTS; PRO00365; AAK94668; 1.

748 RPRINTS; PRO00159; WW\_DOMAIN\_1; 4.

749 RPRINTS; PRO00159; WW\_DOMAIN\_2; 2.

750 RPRINTS; PRO00237; HECT; 1.

Query Match      31.9%;    Score 1239;    DB 4;    Length 922;  
 best Local Similarity      32.5%;    Pre. No. 6.8e-93;  
 matches 300;    Conservative 138;    Mismatches 262;    Indels 224;    Gaps 25;

5 IKIRITYLCAKNLAKDFFRILEDPPFKAVIYDGGQHQHSDPTVK-NTLDPKHNQHYDLYV 62  
 : ::|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 18 LQQVTTSSAKLKRNWFGTA-IYEVVVDG---EITTAKSSESPKNDQEQLTVNV 72

63 GKDTSITISWANHKKIKKQGAGFLG-----CVRLSNAIRBLKD----- 102  
 : :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 73 TPQTLBQWWSHRTL--KA DALLGKATIDLKQALIHNRLKLERKEQIKLISLENXNGI 129

103 --TG-----YORDLICKAAPS-----DTAVRGQIVVSLQTDRI---GTCG- 139  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 130 AQTGELTVLTDGIVIEQENITICSSSPTIEQENGIALHENGEPARTTARLAVEGTNGI 189

140 -SVYDCRGILNEGTYYEDSGPGRPLSCFM----EEPAP-----Y 174  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 190 DNHYPTSTLVQNSCCSYVNGNTTPSSQVAARPNTPAKPLASEPADDTYNGESSSF 249

175 TDSIGAANGC-----GNC-----RFVBEPSQDQRLOQQR 203  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 250 APTONASVTGTPVSEENALSPCTCTTSDPPQFILTSJENNCEIPSTSABEBSEARS 309

204 LRNPDVRSIQT----PQNRPHGHQSP-----ELPEGYEQRTVQGOVYFH 246  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 310 ILBDTSNRSSSAAFEAKSRQDFGCMDFVRQSGNANTETLPSGWEMQRKDPHGRTYYVD 369

247 TGTGVSTWDPR-IP----- 260

370 HNTRTTTWERPOPULPGMERRVDDRRVVYYDHNTTTTWQRPMTESVRNFEBQQSQRNQ 429

261 -----RDINSVNC----DEGLGLPPWNEVTSVSRIFDNRRTTQDPL 305  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 430 LGQAMQNONRYLYSASMIAAENDPYGPLPPWKEVDRSTERVPTPHNTKTQWEDPRT 489

306 HTINHQ-----COLKEPSOPLPLPSEGSLDEELPQARY 340  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 490 QGLQKEPEPEGWIRYREGVYFVDINTRTTFDPNQKSSWYKGG----PQIAY 543

341 ERDLVQKLKVLRLHLSLQQPAQHCRTEVSREBFEESEYRQTMKHPKDLKLRMLMKFRG 400  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 544 ERGFFWKLAHFRY-LCQSNALPShVKNSVSQLFEDSFQQIMALPKYDURRLIVIFRG 602

401 EGGLYGTYAREMYLICHEMLNPYGLFOYSTDNTYMLQINPDSAINPDHLSYFHFGCR 460  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 603 BEGLYGGIAREWFLLSPEBVNPYCILFEYAKRNNTCLQNPASTNPDLISYCFIGR 662

461 IMGLAVPHGHYINGGFTPFYKQKLGKPIQSLDSEYDPELHKSLWILENDITY-LDH 519  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 663 FIANMLFGRGFIDGFSLFYKCNMLSKKLTIDLESITBPNLWIRDNNIEBGLEM 722

520 TFCVBNAAFRGILQHELPKNGRATPVTEENKKEYVRLYVNRFMRGLEAQFLALOGFNE 579  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 723 YFSVDMELLGKVTSHDLKUGGSNTLIVTEENKDYBIGLMTEFRSRYQEQTKAFLDFGFNE 782

580 LIPQHLLKPFQKELELIGGLDKIDLANDWKSNTRLXCVADSNIWRWMAVEFDEER 639  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 783 VVPLQWQYDEKELEVMLCGMQEVLDWQRTVYHTRANSQIWIWQEVKETDNEY 842

640 RARLQFVTGSTRVPLQGXALGSTGARGPRLFTIHLADANTDNLPKAHTCENRDIIPP 699  
 : |:||:||:||:||:||:||:||:||:||:||:||:||:  
 843 RMRLLQFVTGICRLLGGFAELMSSN--GPQRCFCEKVGDT-WLRSHTCENRDLPP 898

700 YESYKLYEKLLTAVETCGFAVE 723  
 : |:||:||:||:||:||:||:||:  
 899 YKSYEOLKEKLFAEBTBEGFGQ3 922

SUMMARIES				
Line No.	Score	Query	Length DB ID	Description
1	4038	100.0	748 22 AAB31477	Amino acid sequence of a human Smurf2 polypeptide.
2	4031	99.8	748 18 AAU19334	Smurf1; Smurf2; Smad signal transduction; bone morphogenic protein; BMP; transforming growth factor-beta; human; TGF-beta; Chondrogenesis; osteogenesis; blood differentiation; cartilage formation; hair growth; neural tube patterning; retinal development; heart induction; KWF; morphogenesis; tooth formation; gamete formation.
3	4027	99.7	804 22 AAU19610	Human protein SEQ
4	3001	74.3	722 24 AAB32274	Novel protein SEQ
5	3001	74.3	723 22 AAB31476	Novel central nerv
6	2992	74.1	722 22 AAM79861	Drosophila melanogaster protein
7	2775	68.7	514 22 AAU87201	Human protein ubiq
8	1545	53.8	1035 22 ABP61120	Aspergillus fumigatus NEDD4 long form
9	1545	38.3	766 18 AAU13385	Aspergillus fumigatus KIAA0439 protein.
10	1530	5	37.9 832 23 ABP73459	Candida albicans e
11	1453	5	36.0 869 24 ABP6104	Aspergillus fumigatus ZGCBP1 prote
12	12	1387	34.3 975 20 AAU93167	Novel human gene,
13	13	1355	33.6 724 18 AAW36797	Human KIAAN ligase
14	14	1354.5	33.5 927 20 AAY25570	Human NEDD4 long f
15	15	1354.5	33.5 927 24 AAE32225	Diseased kidney ti
16	16	1353.5	33.5 995 24 AAE32219	Aspergillus fumigatus
17	17	1353	33.5 923 22 ABG16100	Murine B3 ubiquitin
18	18	1348	33.4 834 23 AAU77175	Drosophila melanogaster
19	19	1340.5	33.2 759 24 ABB25504	Novel human diagno
20	20	1338.5	33.1 854 24 ABP58332	Atrophin-1 interac
21	21	1336	33.1 854 20 AAY3049	Human atrophin-1
22	22	1333	33.0 949 22 ABB59631	Atrophin-1 interac
23	23	1333	33.0 949 22 ABB59556	Drosophila melanogaster
24	24	1329	32.9 852 20 AAY30448	Human E3 ubiquitin
25	25	1301	32.2 739 22 ABG16177	Nedd-4-like ubiquitin
26	26	1301	32.2 739 22 AAG68173	Novel human diagno
27	27	1301	32.2 739 24 ABR41997	Atrophin-1 interac
28	28	1301	32.2 739 24 AAE32270	Human atrophin-1
29	29	1298.5	32.2 870 22 AAE05195	Novel human diagno
30	30	1298.5	32.2 870 24 AAE32222	Human ubiquitin PR
31	31	1297	32.1 922 22 AAB50049	Novel human diagno
32	32	1297	32.1 922 23 ABB05708	Human signal trans
33	33	1285.5	31.8 906 18 AAW36795	Novel human protein
34	34	1281	31.7 733 22 AAB50048	Novel human protein
35	35	1273	31.5 1071 22 ABG11772	Novel human diagno
36	36	1271	31.5 818 18 AAW13386	Human protein ubiq
37	37	1265.5	31.3 1082 22 ABB63355	Drosophila melanogaster
38	38	1209	29.9 474 20 AAY30493	Amino acid sequenc
39	39	1134.5	28.1 683 18 AAW36794	Novel human protein
40	40	1134	28.1 683 22 AAE05194	Novel human protein
41	41	1134.5	28.1 684 24 AAE32221	Human ubiquitin PR
42	42	1092	27.0 1572 23 ABB97662	Nedd-4-like ubiquitin
43	43	1072	26.5 335 22 AAM78877	Novel human protein
44	44	1050	26.0 1562 22 ABG22793	Novel human diagno
45	45	1050	26.0 1562 24 AAE32223	KIAA0322 protein.
ALIGNMENTS				
RESULT 1				
ID AAB31477 standard; Protein: 748 AA.				
XX AAB31477;				
XX DT 20-APR-2001 (first entry)				
XX DE Amino acid sequence of a human Smurf2 polypeptide.				
XX PR 21-DEC-2000.				
XX PF 12-JUN-2000; 20000WO-US16250.				
XX PR 11-JUN-1999; 99US-0138969.				
XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX PA (HSCR-) HSC RES & DEV LP.				
XX P1 Thomsen GH, Warana J;				
XX XX Homo sapiens.				
XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PN 21-DEC-2000.				
XX XX PR 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				
XX XX PR 11-JUN-1999; 99US-0138969.				
XX XX PA (UYNY ) UNIV NEW YORK STATE RES FOUND.				
XX XX PA (HSCR-) HSC RES & DEV LP.				
XX XX P1 Thomsen GH, Warana J;				
XX XX XX XX WO2007168-A2.				
XX XX PN WO2007168-A2.				
XX XX PR 21-DEC-2000.				
XX XX PF 12-JUN-2000; 20000WO-US16250.				

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

N-PSDB; AAF24853.

Novel isolated Smurf protein useful for inhibiting bone morphogenic protein or tumor growth factor-beta activation pathway, for treating cancer and to block osteogenesis, hair growth, tooth formation -

Claim 10; Fig 12; 107pp; English.

The present sequence represents a human Smurf2 polypeptide. The specification also describes a Smurf1 polypeptide. Smurf polypeptides are negative regulators of Smad signal transduction, and antagonists of bone morphogenic protein (BMP) or transforming growth factor-beta (TGF-beta) signalling pathway. Expression of Smurf1 in a cell is useful for inhibiting BMP or TGF-beta activation pathway in a cell. Smurf polypeptides are useful for blocking chondrogenesis, osteogenesis, blood differentiation, cartilage formation, neural tube patterning, retinal development, heart induction and morphogenesis, hair growth, tooth formation, gamete formation and a wide variety of tissue and organ formation processes, and hinder the regeneration, growth, maintenance, etc., of bone and other tissues that are dependent on the BMP pathway. The polypeptide is useful for screening for various drugs and/or antibodies that can either enhance the BMP pathway, or inhibit it.

Sequence 748 AA;

Query Match	100.0%	Score 4038;	DB 22;	Length 748;
est Local Similarity	100.0%	Pred. No. 0;		
atches 748;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1 MSNPGRNRNGPKVLRITVICAKNLVKPDKFRLLDPDFEKFVVDGSGQCHSTDTVKNTLDPK 60				
1 MSNPGRNRNGPKVLRITVICAKNLVKPDKFRLLDPDFEKFVVDGSGQCHSTDTVKNTLDPK 60				
61 WNCQHYDLYIGKSDSUTTISWNCKTHKQAGAGLGCUTLISMAINIKDGTQYQLDCKL 120				
61 WNCQHYDLYIGKSDSUTTISWNCKTHKQAGAGLGCUTLISMAINIKDGTQYQLDCKL 120				
121 GPNDNDTVRGOIVVLSLQRDRIGTGQVQVDCSRLFDNDLDPGMERETASGRIQYLNHIT 180				
121 GPNDNDTVRGOIVVLSLQRDRIGTGQVQVDCSRLFDNDLDPGMERETASGRIQYLNHIT 180				
181 RTTQWERTPBASEYSSGRPLSCDVDENTPISTGNTGATCGQSSDPRLAERRRSRHRN 240				
181 RTTQWERTPBASEYSSGRPLSCDVDENTPISTGNTGATCGQSSDPRLAERRRSRHRN 240				
241 YMSRTHLHTPDLPEGYEORTTOQQVYFLHTCTGVSTWHDPVPRLSNINCEELGPLP 300				
241 YMSRTHLHTPDLPEGYEORTTOQQVYFLHTCTGVSTWHDPVPRLSNINCEELGPLP 300				
301 PGWEINTNTATGRVYTDHNRRRTQDPRLSANHLVNQNOLKDQQQQVVSICPDDT 360				
301 PGWEINTNTATGRVYTDHNRRRTQDPRLSANHLVNQNOLKDQQQQVVSICPDDT 360				
361 ECLTVPRYKDLVOKLKLRLQELSQQPQAGHCIEVSREEFEESTRVNKMRPKD LWK 420				
361 ECLTVPRYKDLVOKLKLRLQELSQQPQAGHCIEVSREEFEESTRVNKMRPKD LWK 420				
421 RLMIKRGERGEGLDGCVARWNLILSHEMLNPyGLFQYSRDIYIYTQINPDSAVNPEHL 480				
421 RLMIKRGERGEGLDGCVARWNLILSHEMLNPyGLFQYSRDIYIYTQINPDSAVNPEHL 480				
481 SYFHFGRIMGMAVFGHYIDGGFTLPFYKQLLGKSITLDDMBLVDPDLANSLWILEND 540				
481 SYFHFGRIMGMAVFGHYIDGGFTLPFYKQLLGKSITLDDMBLVDPDLANSLWILEND 540				
541 ITGVLDLHTFCVHNAYGEIQHELKPGKGSIPYNEENKEYTYRLVYNWRFLRGIAQFLA 600				
541 ITGVLDLHTFCVHNAYGEIQHELKPGKGSIPYNEENKEYTYRLVYNWRFLRGIAQFLA 600				
601 LOKGMEVJEPHLLKTFDEKELELJIGIGKIDYNDKVNTRLKHCPDSDNIVKMFWKAV 660				
601 LOKGMEVJEPHLLKTFDEKELELJIGIGKIDYNDKVNTRLKHCPDSDNIVKMFWKAV 660				

Query	661 EFPDEERARRLIQFFVTGSSRVPLQQFKALQGAAGPRLFIHQIDACTNNLPAKHTCFNRI 720
Db	661 EFPDEERARRLIQFFVTGSSRVPLQQFKALQGAAGPRLFIHQIDACTNNLPAKHTCFNRI 720
Query	721 DIPPYESYEKLYEKLLTAIEBTGFAVE 748
Db	721 DIPPYESYEKLYEKLLTAIEBTGFAVE 748
RESULT 2	
ID	AAW13384 standard; Protein; 748 AA.
XX	
AC	AAW13384;
XX	
DT	10-JUL-1997 (First entry)
XX	
DB	Human protein ubiquitin ligase publ.
XX	
KW	Protein ubiquitin ligase; publ; cdc25 phosphatase; CDK kinase; p53; cell cycle; transgenic animal.
XX	
OS	Homo sapiens.
XX	
PN	W09712362-A1.
XX	
PD	10-APR-1997.
XX	
PF	04-OCT-1996;
XX	96WO-US15930.
PR	04-OCT-1995;
XX	95US-0539205.
PA	(COLD-) COLD SPRING HARBOR LAB.
XX	
PI	Beach D, Caliguri M, Nefsky B;
XX	
DR	WPI; 1997-226206/20.
N-PSDB; AAT7040.	
PS	Claim 1; Page 74-77; 108pp; English.
XX	
CC	Human protein ubiquitin ligases publ (AAW13385), Pub2 (AAW13384), and pub3 (AAW13386) are homologues of fission yeast pub1 (AAW13387) and were identified from cDNA clones (AAT7040-02) obtcd. e.g. from a keratinocyte cDNA library. Pub polypeptides can be produced in transfected host cells. They can control the steady state level of cdc25 phosphatase, the degree of CDK kinase (e.g. cdkc) dephosphorylation and the steady state level of p53 (controlling the degree of cell cycle regulation of cell growth or proliferation by cell or tissue differentiation, or a specific (ant)agonist of wild-type protein function and may be used as immunogens to elicit a specific immune residue.
XX	
SQ	Sequence 748 AA;
Query	99.8%; Score 4031; DB 18; Length 748;
Best Local Similarity	99.9%; Pred. No. 0;
Matches	747; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	1 MSNPGRNRNGPKVLRITVLCNLYKDFPRLPDFAKTVVGDGSQCHSTDTVKNTLDPK 60
Query	1 MSNPGRNRNGPKVLRITVLCNLYKDFPRLPDFAKTVVGDGSQCHSTDTVKNTLDPK 60
Db	61 WNCQHYDLYIGKSDSUTTISWNCKTHKQAGAGLGCUTLISMAINIKDGTQYQLDCKL 120
Query	61 WNCQHYDLYIGKSDSUTTISWNCKTHKQAGAGLGCUTLISMAINIKDGTQYQLDCKL 120
Db	121 GPNDNDTVRGOIVVLSLQRDRIGTGQVQVDCSRLFDNDLDPGMERETASGRIQYLNHIT 180
Query	121 GPNDNDTVRGOIVVLSLQRDRIGTGQVQVDCSRLFDNDLDPGMERETASGRIQYLNHIT 180
Db	181 RTTQWERTPBASEYSSGRPLSCDVDENTPISTGNTGATCGQSSDPRLAERRRSRHRN 240
Query	181 RTTQWERTPBASEYSSGRPLSCDVDENTPISTGNTGATCGQSSDPRLAERRRSRHRN 240
Db	241 YMSRTHLHTPDLPEGYEORTTOQQVYFLHTCTGVSTWHDPVPRLSNINCEELGPLP 300
Query	241 YMSRTHLHTPDLPEGYEORTTOQQVYFLHTCTGVSTWHDPVPRLSNINCEELGPLP 300
Db	301 PGWEINTNTATGRVYTDHNRRRTQDPRLSANHLVNQNOLKDQQQQVVSICPDDT 360
Query	301 PGWEINTNTATGRVYTDHNRRRTQDPRLSANHLVNQNOLKDQQQQVVSICPDDT 360
Db	361 ECLTVPRYKDLVOKLKLRLQELSQQPQAGHCIEVSREEFEESTRVNKMRPKD LWK 420
Query	361 ECLTVPRYKDLVOKLKLRLQELSQQPQAGHCIEVSREEFEESTRVNKMRPKD LWK 420
Db	421 RLMIKRGERGEGLDGCVARWNLILSHEMLNPyGLFQYSRDIYIYTQINPDSAVNPEHL 480
Query	421 RLMIKRGERGEGLDGCVARWNLILSHEMLNPyGLFQYSRDIYIYTQINPDSAVNPEHL 480
Db	481 SYFHFGRIMGMAVFGHYIDGGFTLPFYKQLLGKSITLDDMBLVDPDLANSLWILEND 540
Query	481 SYFHFGRIMGMAVFGHYIDGGFTLPFYKQLLGKSITLDDMBLVDPDLANSLWILEND 540
Db	541 ITGVLDLHTFCVHNAYGEIQHELKPGKGSIPYNEENKEYTYRLVYNWRFLRGIAQFLA 600
Query	541 ITGVLDLHTFCVHNAYGEIQHELKPGKGSIPYNEENKEYTYRLVYNWRFLRGIAQFLA 600
Db	601 LOKGMEVJEPHLLKTFDEKELELJIGIGKIDYNDKVNTRLKHCPDSDNIVKMFWKAV 660
Query	601 LOKGMEVJEPHLLKTFDEKELELJIGIGKIDYNDKVNTRLKHCPDSDNIVKMFWKAV 660
Db	661 GPNDNDTVRGOIVVLSLQRDRIGTGQVQVDCSRLFDNDLDPGMERETASGRIQYLNHIT 180
Query	661 GPNDNDTVRGOIVVLSLQRDRIGTGQVQVDCSRLFDNDLDPGMERETASGRIQYLNHIT 180

121	GPNDNDTIVRQOLVVSLQSQRDRGTCGGYVDSRPLAERVRSSRHNHIT	180
181	RTTQWBRPTRPASEYSSGRPLSCFVDNTPLSGINGATCGOSSPDRLAERVRSSRHN	240
181	RTTQWBRPTRPASEYSSGRPLSCFVDNTPLSGINGATCGOSSPDRLAERVRSSRHN	240
241	YMSRTHIHTPPDLPEGYBQRTTOQQQYYFLHTQTGYSTWHDRVPRLSNINCEEGPLP	300
241	YMSRTHIHTPPDLPEGYBQRTTOQQQYYFLHTQTGYSTWHDRVPRLSNINCEEGPLP	300
301	PGWEIRNTATGEVVFYDHNNRTTQFDPRISANLHIVLNROQNLKQQQQVYSICPDPT	360
301	PGWEIRNTATGEVVFYDHNNRTQFDPRISANLHIVLNROQNLKQQQQVYSICPDPT	360
361	ECLTVPRYKRDLVQKLLKILRQLPSQOPOAGHCRIEVSREELFEESYRQNMKRPDLWK	420
361	ECLTVPRYKRDLVQKLLKILRQLPSQOPOAGHCRIEVSREELFEESYRQNMKRPDLWK	420
421	RIMIKPRGEGEGLDGGYAREWLYLISHEMANPYGYFOYSRDIYLQINPDSAYNPEHL	480
421	RIMIKPRGEGEGLDGGYAREWLYLISHEMANPYGYFOYSRDIYLQINPDSAYNPEHL	480
481	SYFHFGVRIGMVAWFHGTYIDGGFTLPFYKQOLGKSTLDDMELVDPDLRNSLVNLLEND	540
481	SYFHFGVRIGMVAWFHGTYIDGGFTLPFYKQOLGKSTLDDMELVDPDLRNSLVNLLEND	540
541	ITGVLDIHTFCVHNAGEBIIQHELKNGKSIPVNENKKEYVRLYNNWRFLRGIEQFLA	600
541	ITGVLDIHTFCVHNAGEBIIQHELKNGKSIPVNENKKEYVRLYNNWRFLRGIEQFLA	600
601	LQKGFNEVIPQHLLKTDEKELELICLGKTDVNNDKVNTRLKHCTPDSNIVKWFKA	660
601	LQKGFNEVIPQHLLKTDEKELELICLGKTDVNNDKVNTRLKHCTPDSNIVKWFKA	660
661	EFFDEERARLILQFTVQFVTSRVPLOGKALOGAAQPLFTIFHQIDACTNNLPLKAHTCFNRI	720
661	EFFDEERARLILQFTVQFVTSRVPLOGKALOGAAQPLFTIFHQIDACTNNLPLKAHTCFNRI	720
721	DIPPYEEYEXKLITAEKLTIAETCGFAVE	748
721	DIPPYEEYEXKLITAEKLTIAETCGFAVE	748

AAU19610 AAU19610 Standard; protein; 804 AA.  AAU19610;	04-DEC-2001 (first entry)	Human diagnostic and therapeutic polypeptide (DITHP) #196.  Human; receptor; diagnostic; therapeutic; gene therapy; vascular cell proliferative disorder; Crohn's disease; lymphoma; leucocyte; acquired immune deficiency syndrome; AIDS; autoimmune disease; respiratory disorder;
JULT 3 19610		

Ergonomics

NOZU 19292 / -A2.

30-AUG-2001.

2001 - FEB - 2001 : 200

~~EE4 - FEB = 2000;~~ 2000

24-FEB-2000; 200

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24-FEB-2000; 200

PPR	24-FEB-2000;	2000US10184771;
PPR	24-FEB-2000;	2000US10184772;
PPR	24-FEB-2000;	2000US10184773;
PPR	24-FEB-2000;	2000US10184776;
PPR	24-FEB-2000;	2000US10184777;
PPR	24-FEB-2000;	2000US10184777;
PPR	24-FEB-2000;	2000US10184797;
PPR	24-FEB-2000;	2000US10184813;
PPR	24-FEB-2000;	2000US10184837;
PPR	24-FEB-2000;	2000US10184841;
PPR	24-FEB-2000;	2000US10184841;
PPR	24-FEB-2000;	2000US10185213;
PPR	24-FEB-2000;	2000US10185216;
PPR	12-MAY-2000;	2000US1020385;
PPR	15-MAY-2000;	2000US10204226;
PPR	16-MAY-2000;	2000US10204525;
PPR	16-MAY-2000;	2000US10204526;
PPR	16-MAY-2000;	2000US10204908;
PPR	16-MAY-2000;	2000US10205232;
PPR	17-MAY-2000;	2000US10204863;
PPR	17-MAY-2000;	2000US10205221;
PPR	17-MAY-2000;	2000US10205285;
PPR	17-MAY-2000;	2000US10205286;
PPR	17-MAY-2000;	2000US10205287;
PPR	17-MAY-2000;	2000US10205323;
PPR	17-MAY-2000;	2000US10205324.
		(INCY-) INCYTE GENOMICS INC.
		Panzer SR., Spiro PB., Barvil Chen A., D'Sa SA., Amshay S. Dufour GE., Flores V., Fong W. Liu TP., Roseberry AM., Rosen Wright RJ., Yap PE., Yu JY, Cohen HJ., Hodson DM., Lincoff
		WPI: 2001-502867/55. N-PSDB; AS31181.
		Polynucleotides encoding diag enzymes, hormones and receptors
		-
		Claim 27: Page 512-514; 522DPB
		The invention relates to poly therapeutic (DITHP) polypepti and proteins involved in grow associated with inappropriate (II) may be used to produce th expression by rectifying muta that affect the activity of t or supplementing the patient's may be used to treat diseases Crohn's disease, acquired immu samples, and therefore which (I) may be used to produce th into a host cell and culturing its complementary sequences m assays to detect and quantit samples, and therefore which (II) may also be used as antibodies against DITHPs and expression and activity. The also be used to down regulate antibodies may also be used as presence of DITHPs in samples assay (ELISA). AAU19415-AAU1 therapeutic (DITHP) polypepti sequence 804 AA:

Query Match Score 4027; DB 22; Length 804;  
 1st Local Similarity 99.7%; Pred. No. 0;  
 Itches 746; Conservation 0; Mismatches 2; Indels 0; Gaps 0;  
 XX WO200290549-A2.  
 1 MSNPGRNRNGPVKLRTVLCANLKVKEFFRLPDPFARKVVDGSGCCHSTPTVKNTLDPK 60  
 57 MSNPSSRNPVKHLTVLCAKNVKDFEFLDPFARKVVDGSGCCHSTPTVKNTLDPK 116  
 61 WQHYDLYIGKSDSVTISWNHKKIKTKQAGELGCVLLSNAINKDGTQYQRLCKL 120  
 117 WQHYDLYIGKSDSVTISWNHKKIKTKQAGELGCVLLSNAINKDGTQYQRLCKL 176  
 121 GPNDNTDVTROQIVNSLQSDRIGTGGTQDCSFLFDNLDPDWEERTASGRIQYLNHIT 180  
 177 GPNDNTDVTROQIVNSLQSDRIGTGGTQDCSFLFDNLDPDWEERTASGRIQYLNHIT 236  
 181 RTTOWERPRTPASEYSSPRPLSFVDEDTPISTGNTGATCGOSSDPLAERSVSRHRN 240  
 237 RTTOWERPRTPASEYSSPRPLSFVDEDTPISTGNTGATCGOSSDPLAERSVSRHRN 296  
 241 YMSRTHLHTPDLPPEGYERTTQGQYFLHTOTGVSTWHDPRVPDLSNINCEBGLPLP 300  
 297 YMSRTHLHTPDLPPEGYERTTQGQYFLHTOTGVSTWHDPRVPDLSNINCEBGLPLP 356  
 301 PGWEIRNTATGRVYEDHNNTTODPDLPSANLHLVLRONOLQDCQQQVYSLCPDDT 360  
 357 PGWEIRNTATGRVYEDHNNTTODPDLPSANLHLVLRONOLQDCQQQVYSLCPDDT 416  
 361 ECLTYRKYEDLVQLKILRQLELSQQPOA9HCRIEVSREEFEESYRQNMKMRPKDLWK 420  
 417 ECLTYRKYEDLVQLKILRQLELSQQPOA9HCRIEVSREEFEESYRQNMKMRPKDLWK 476  
 421 RIMIKRGERGEGLDYGGVAREWLYLISHEMINPYGYLFOYSRDIYTLQINPDSAYNPEHL 480  
 477 RLMTRFRGERGEGLDYGGVAREWLYLISHEMINPYGYLFOYSRDIYTLQINPDSAYNPEHL 536  
 481 SYFHVGGRINGMAYFHGHYDGGETLPFYKOLIGSKTLDMDLNUEDDLANSLWMLEND 540  
 537 SYFHVGGRINGMAYFHGHYDGGETLPFYKOLIGSKTLDMDLNUEDDLANSLWMLEND 596  
 541 ITGVLDLHTFCVHNAYGETIQLHEKLRPGKSIPTNEENKEYTRLYNNWRURGIBAQFLA 600  
 597 ITGVLDLHTFCVHNAYGETIQLHEKLRPGKSIPTNEENKEYTRLYNNWRURGIBAQFLA 656  
 601 LQKGPMEVIPOHLLKTDEKELELJIGLGKIDVNDVNTLKEKCTPDSNIVKWFKA 660  
 657 LQKGPMEVIPOHLLKTDEKELELJIGLGKIDVNDVNTLKEKCTPDSNIVKWFKA 716  
 661 EFFDEERRARLQLQFTGSSSRVPLQGKALQGAAGPRLTIHQIDACTNNLPKAHTCFNRI 720  
 717 EFFDEERRARLQLQFTGSSSRVPLQGKALQGAAGPRLTIHQIDACTNNLPKAHTCFNRI 776  
 721 DIPPSYSEKLYEKLLTAETTCGFAVE 748  
 777 DIPPSYSEKLYEKLLTAETTCGFAVE 804

DUT 4  
 AAE332724 standard; Protein; 722 AA.  
 24-MAR-2003 (first entry)  
 E3 ubiquitin ligase SMURF1 protein.  
 Viral infection; lymphosarcoma; human immunodeficiency virus; hepatitis; poliomyelitis; HIV; measles; protein therapy; E3 ubiquitin ligase; Unidentified.

Query Match Score 3001; DB 24; Length 722;  
 Best Local Similarity 74.3%; Pred. No. 3 8e-274;  
 Matches 565; Conservative 63; Mismatches 71; Indels 58; Gaps 8;  
 XX DR N-PSDB; AAD50458.  
 12 VCKRLTUVCAKQVKKDFREFLDPDPAKUYVDGSGCCHSTDTVKNTLDPKQHYNHDTGK 71  
 4 IKRLTVLCAKNLAKDFEFLDPDPAKUYVDGSGCCHSTDTVKNTLDPKQHYNHDTGK 63  
 72 SDSVTISWNHKKIKHKQAGFLGCVLLSNAINKDGTQYQRLCKLGPNDNTYRGQ 131  
 64 TDSTISWNHKKIKHKQAGFLGCVLLSNAINKDGTQYQRLCKLGPNDNTYRGQ 123  
 132 IVVSLQEDRIGTGQVVDCSRFLNDLDPGWEERTAAGRQYLNHITRTTOWERPTRP 191  
 124 IVVSLQEDRIGTGGSVUDCRGLLENE-----GTVY----- 154  
 192 ASEYSSPGRPLSCFVDENTPISGTNGATCG-----QSSDERLAERVRQRHRNTM 242  
 155 -EDSGPGRPLSCFEMEPAPYTDSTSAAAGGGNCRFVESPSQDORLQAQRLRPDVRSGL 212  
 243 ----SRPLHHTPPDLPPEGYERTTQGQYFLHTOTGVSTWHDPRVPDLSNINCEBGLP 298  
 213 QTPQNRPGHGOSPELPGIGERTTQGQYFLHTOTGVSTWHDPRVPDLSNINCEBGLP 272  
 299 LPFGWEIRNTATGRVYFDHNNTTODPDLPSANLHLVLRONOLQDCQQQVY---S 354  
 273 LPFGWEIRNTSRYGRLFEDHNNTTODPDLPSANLHLVLRONOLQDCQQQVY---S 328  
 355 LCPBDTECLTYPRYKDLVQKLKVRLQOQPOA9HCRIEVSREEFEESYRQVMKR 414  
 329 L---EDEELPAQRYERDLVQKLKVRLQOQPOA9HCRIEVSREEFEESTQIMKR 365

415 PDKLRLRMLKFRGEGLDGGVAREWLYLSSHEMLNPPYGLFOYSRDDIYTQINPDS 474  
 386 PDKLRLRMLKFRGEGLDGGVAREWLYLSSHEMLNPPYGLFOYSRDDIYTQINPDS 445  
 475 VNPEHISYFHVGRTRGMAVFGHYDGSFTLPFYKQQLGKSTTIDMELVDPDLHSNLV 534  
 446 INPDHISYFHVGRTRGMALVAFGHYDGSFTLPFYKQQLGKSTTIDMELVDPDLHSNLV 505  
 535 WILENDITGULDHRCCEUNAYGETIQHQLPKPGKSI PWNENKVKYVRLYNNRERGI 524  
 506 WILENDITGULDHRCCEUNAYGETIQHQLPKPGKSI PWNENKVKYVRLYNNRERGI 565  
 595 EAQFLAQKGFNEVTPQHILKTDEKELEBLIICLGKDNDMKVNTRLKHTCPDNIVK 654  
 566 EAQFLAQKGFNEVTPQHILKTDEKELEBLIICLGKDNDMKVNTRLKHTCPDNIVK 625  
 655 WFWKAVEFFDEERRARLLQPTVTGSSRVPQGFKAHQ--GAAPRLPTTHQIDACTNINLP 711  
 626 WFWKAVEFFDEERRARLLQPTVTGSSRVPQGFKAHQ--GAAPRLPTTHQIDACTNINLP 685  
 712 KAHTCFNRIDIPPIESYEKUYEKULATAETCGFAVE 748  
 686 KAHTCFNRIDIPPIESYEKUYEKULATAETCGFAVE 722

ULT  
3.476

AAB34476 standard; Protein; 723 AA.

AAB34476;

20-APR-2001 (first entry)

Amino acid sequence of a human Smurf1 polypeptide.

**Smurf1:** Smad signal transduction; bone morphogenic protein; BMP; osteogenesis; blood differentiation; human; tgf-beta; chondrogenesis; neural tube patterning; cartilage formation; hair growth; neural tube patterning; retinal development; heart induction; morphogenesis; tooth formation; gamete formation.

Homo sapiens.

WO200007168-A2.  
21-DEC-2000.

12-JUN-2000; 20000W0-US16250.

11-JUN-1999; 99US-0138069.

(UNIV NEW YORK STATE RES FOUND.  
(HSCR-) HSC RES & DEV LP

Thomsen GH, Wrama J;  
WPI; 2001-071267/08.  
N-PSDB; AAT24852;

Novel isolated Smurf protein useful for inhibiting bone morphogenic protein or tumor growth factor-beta activation pathway, for treating cancer and to block osteogenesis, hair growth, tooth formation -

Claim 6; Fig 10; 107pp; English.

The present sequence represents a human Smurf1 polypeptide. The specification also describes a Smurf2 polypeptide. Smurf polypeptides are negative regulators of Smad signal transduction, and antagonists of bone morphogenic protein (BMP) or transforming growth factor-beta (TGF-beta) signalling pathway. Expression of Smurf1 in a cell is useful for inhibiting a BMP or TGF-beta activation pathway in a cell. Smurf polypeptides are useful for blocking chondrogenesis, osteogenesis, blood differentiation, cartilage formation, neural tube patterning, retinal

CC	development, heart induction and morphogenesis, hair growth, tooth formation, gamete formation and a wide variety of tissue and organ
CC	formation processes, and hinder the regeneration, growth, maintenance, etc., of bone and other tissues that are dependent on the BMP pathway.
CC	The polypeptide is useful for screening for various drugs and/or antibodies that can either enhance the BMP pathway, or inhibit it.
XX	
SQ	Sequence 723 AA;
Query	Query Match 74.1%; Score 3001; DB 22; Length 723; Best Local Similarity 74.3%; Pred. No. 3.9e-274; Matches 565; Conservative 63; Mismatches 71; Indels 58; Gaps 8;
Db	12 VKLRLTVLCARNLVKEDFRLDPDFAKVYVDGSGCQHSTDVQNTLDPKRNQHYDLYRK 71 5 IKRLTVLCARNLAKEDFRLDPDFAKVYVDGSGCQHSTDVQNTLDPKRNQHYDLYRK 64
Qy	72 SPSVTISWNHRKHKQGAGFLGCYRLSNAINFLKDTCYQRDLCKLGFDNDTDRVQO 131 65 TDSTISWNHRKHKQGAGFLGCYRLSNAISLKDTCYQRDLCKUNPSDDAVRQO 124
Qy	132 IVSLSQSDRIGTGQYVDCSRLFLNDLPDGWEERTARTASGRIQVLNHITRTTOWERPPTP 191 125 IVSLSQSDRIGTGQYVDCSRLFLNDLPDGWEERTARTASGRIQVLNHITRTTOWERPPTP 155
Db	192 ASEYSSPPLSPCPVDETDPTSGTNGATCG-----QSSDPPLAERRVRSSORHRYM 242 156 --EDSGPGRPLSCMFERPAPYDTSGAAAGGNCFVESEPSQDQRLOAQRLNFDVRGSL 213
Qy	243 ---SRYALHTPPDLPGYEORTTQGQYVFLHTQGWSWHDPVPRPLSNTNCDELGP 238 214 QTPQNRPGRHQSPELPPEGYQRTTYQGQYVFLHTQGWSWHDPRPLNSYNODELGP 273
Db	299 LCPDDTECLTVPRYKRDVLQVKLKIQLRQELSQQPAQHCRIEVSREETFEESYRQVMKR 414 274 LPPOWEVSTVSGRIVYFQDHNRTTOFTDER-LHHIMNHOCOLKEPSQPLPSEGS 329
Qy	355 LCPDDTECLTVPRYKRDVLQVKLKIQLRQELSQQPAQHCRIEVSREETFEESYRQVMKR 414 330 L--EDELPARYERILVQKLKVHLELSQQPAQHCRIEVSREETFEESYRQVMKR 366
Db	415 PKDIWKRMIXKPRGEEGSDYGEVAREWLYLISHEMLNPPYGLFOYSRDTIYTQINPDSA 474 387 PKDIWKRMIXKPRGEEGSDYGEVAREWLYLICHENLNPPYGLFOQSTDNLYMLOINPDS 446
Qy	475 VNDPHLSFHFYCRIMMAVFGHIDGCFTLPLFYKQOLIKSITLDDMLLVDPLENSV 514 447 INPHSHLSYFHYGRIMGLAVFHYINGGFVPPFKQOLQSKPIQOLSDLSVDPLHKSIV 505
Db	535 WILDENDITGVLDTFCYEHNAYGEI QHELKPGNGKSIPNBNENKEYYLYVNRPLRJ 594 507 WILDENDITPVLDHTFCYEHNAYGEI QHELKPGNGKSIPNBNENKEYYLYVNRPLRJ 566
Qy	595 EAQFLALOKGENEVIPQHLLTFDEKELELIGGKIDNDWKNTNRLHCTPDSDNIVK 654 567 EAQFLALOKGENELIPQHLLTFDEKELELIGGKIDNDWKNTNRLHCTPDSDNIVK 626
Db	655 WFYKAVERFDEERRARLLQFTGSSRVPLQGKFALQ-GAAGPPLFTIHQIDACTNNILP 711 627 WFYKAVERFDEERRARLLQFTGSSRVPLQGKFALQ-GAAGPPLFTIHQIDACTNNILP 686
Qy	712 KAHTCFNRIDIPPIESYEKULATAETCGFAVE 748 687 KAHTCFNRIDIPPIESYEKULATAETCGFAVE 723
Db	

RESULT 6  
AAM79861  
ID AAM79861 Standard; Protein; 722 AA.  
XX  
AC AAM79861;  
DT 06-NOV-2001 (first entry)



16-MAR-2000; 2000US-0189874.  
 17-MAR-2000; 2000US-0190075.  
 18-APR-2000; 2000US-0198123.  
 19-MAY-2000; 2000US-0205515.  
 20-JUN-2000; 2000US-0209467.  
 28-JUN-2000; 2000US-0214886.  
 30-JUN-2000; 2000US-0215135.  
 07-JUL-2000; 2000US-0216447.  
 07-JUL-2000; 2000US-0216880.  
 11-JUL-2000; 2000US-0217487.  
 11-JUL-2000; 2000US-0217496.  
 14-JUL-2000; 2000US-0218290.  
 26-JUL-2000; 2000US-0220963.  
 26-JUL-2000; 2000US-0220964.  
 14-AUG-2000; 2000US-0224518.  
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 14-AUG-2000; 2000US-0225213.  
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 14-AUG-2000; 2000US-0225757.  
 14-AUG-2000; 2000US-0225758.  
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 22-AUG-2000; 2000US-0226681.  
 22-AUG-2000; 2000US-0226868.  
 22-AUG-2000; 2000US-0227182.  
 22-AUG-2000; 2000US-0227009.  
 30-AUG-2000; 2000US-0228924.  
 01-SEP-2000; 2000US-0229287.  
 01-SEP-2000; 2000US-0229343.  
 01-SEP-2000; 2000US-0229344.  
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 08-SEP-2000; 2000US-0231242.  
 08-SEP-2000; 2000US-0231244.  
 08-SEP-2000; 2000US-0231244.  
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 08-SEP-2000; 2000US-0232080.  
 08-SEP-2000; 2000US-0232081.  
 12-SEP-2000; 2000US-0231968.  
 14-SEP-2000; 2000US-0232397.  
 14-SEP-2000; 2000US-0232398.  
 14-SEP-2000; 2000US-0232399.  
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 14-SEP-2000; 2000US-0233063.  
 14-SEP-2000; 2000US-0233064.  
 21-SEP-2000; 2000US-0233065.  
 21-SEP-2000; 2000US-0234223.  
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 02-OCT-2000; 2000US-0236802.  
 02-OCT-2000; 2000US-0237037.  
 02-OCT-2000; 2000US-0237038.  
 02-OCT-2000; 2000US-0237039.  
 02-OCT-2000; 2000US-0237040.

13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
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 PR 01-NOV-2000; 2000US-0244617.  
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 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
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 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
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 PR 08-NOV-2000; 2000US-0246528.  
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 PR 08-NOV-2000; 2000US-0246609.  
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 PR 08-NOV-2000; 2000US-0249208.  
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 PR 08-NOV-2000; 2000US-0249220.  
 PR 08-NOV-2000; 2000US-0249221.  
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 PR 08-NOV-2000; 2000US-0249297.  
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 PR 01-DEC-2000; 2000US-025160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 06-DEC-2000; 2000US-0251719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0251097.  
 PR 05-JAN-2001; 2001US-0255678.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Rosen CA, Barash SC, Ruben SM;  
 XX DR WPI; 2001-581633/65.  
 DR N-PSDB; ABK43631.  
 XX New isolated nucleic acid encoding a protein for diagnosing,  
 PT preventing, treating or ameliorating medical conditions and used as  
 PT food additives or preservatives -  
 XX Claim 9; SEQ ID No 819; 837pp; English.  
 PS

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical condition and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cerebral ischaemia, e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. cornual infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, very Match 68.7%; Score 2775; DB 22; Length 514; best Local Similarity 99.8%; Pred. No. 5.2e-253; Mismatches 1; Indels 0; Gaps 0; attaches 513; Conservative 1; Sequence Listing -

235 SORHRNTMSRTHLHTPDLPEGYERQTTOQGQVFLHTQGSTWHDRVRPDLNSNCE 294  
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 1 SRRHRTMSRTHLHTPDLPEGYERQTTOQGQVFLHTQGSTWHDRVRPDLNSNCE 60  
 295 ELPGLPPGMEWTRNTATGRYVFDHNRTRTQFTDPRLSANLHLVLRNQNQLDQQQQYVS 354  
 |||||:|||:|||:|||:|||:|||:|||:|||:  
 61 ELPGLPPGMEWTRNTATGRYVFDHNRTRTQFTDPRLSANLHLVLRNQNQLDQQQQYVS 120  
 355 LCPDDTECBLTPRYKEDLVQKLKIRQELSQQQPAQHCRIEVSREEFEESYRQNMKR 414  
 |||||:|||:|||:|||:|||:|||:  
 121 LCPDDTECBLTPRYKEDLVQKLKIRQELSQQQPAQHCRIEVSREEFEESYRQNMKR 180  
 415 PXLDMRKLMIKPRGEGLDYGVARWLYLISHENLNPYGLFOYSRDDIYTQINDSA 474  
 |||||:|||:|||:|||:|||:  
 181 PXLDMRKLMIKPRGEGLDYGVARWLYLISHENLNPYGLFOYSRDDIYTQINDSA 240  
 475 VNEPHLSYFHFGRIMGMAVPHGYIDGGFLPFPYKQLIGKSITLDMDLVLDDLNLSV 534  
 |||||:|||:|||:|||:|||:  
 241 VNEPHLSYFHFGRIMGMAVPHGYIDGGFLPFPYKQLIGKSITLDMDLVLDDLNLSV 300  
 535 WIENDITGVLDTHTFCEHNAYGEILOHELKPNGKSIPIVNEENKKEYVRLYYNWRFRGKI 594  
 |||||:|||:|||:|||:|||:  
 301 WIENDITGVLDTHTFCEHNAYGEILOHELKPNGKSIPIVNEENKKEYVRLYYNWRFRGKI 360  
 595 EAQFLAQKGNEVIPOHLLKTDEKELELLIGKIDNDWKNTLKHCTPDSNVK 654  
 |||||:|||:|||:|||:  
 361 EAQFLAQKGNEVIPQHLLKTDEKELELLIGKIDNDWKNTLKHCTPDSNVK 420  
 655 WFKWAVERPDEEPRARLQFTGSSVPLOOPKALQGAAPRLPTIHQDACTNNLPAH 714  
 |||||:|||:|||:|||:  
 421 WFKWAVERPDEEPRARLQFTGSSVPLOOPKALQGAAPRLPTIHQDACTNNLPAH 480  
 715 TCFNRIDIPPESYEKLYEKULTAIBETCGFAVE 748  
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 481 TCFNRIDIPPESYEKLYEKULTAIBETCGFAVE 514

Drosophila melanogaster polypeptide SEQ ID NO 10152.  
 DB XX Drosophila; developmental biology; cell signalling; insecticide;  
 XX KW pharmaceutical.  
 XX Drosophila melanogaster.  
 OS XX Drosophila melanogaster.  
 PN XX WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PP 23-MAR-2001; 2001WO-US09231.  
 XX PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-1614150.  
 XX PA (PBKE ) PE CORP NY.  
 XX PI Venter JC, Adams M, Li FWD, Myers EW;  
 DR XX WPI; 2001-658860/75.  
 DR N-PSDB: ABL05223.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -  
 PT PT interactions -  
 XX Disclosure; SEQ ID NO 10152; 21PP + Sequence Listing; English.  
 PS XX  
 CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developing cell signalling and elucidating cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutic and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB163051), expressed DNA sequences (AB101840-AB16175) and the encoded proteins (AB55737-AB72072).  
 CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [http://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).  
 CC  
 XX Sequence 1035 AA;  
 Query 53.8%; Score 2173; DB 22; Length 1035;  
 Best Local Similarity 43.2%; Pred. No. 1.4e-194; Mismatches 154; Indels 342; Gaps 16;  
 Matches 455; Conservative 104; Sequence Listing -

Qy 7 RRGPKVKRLTVLAKQNLVKDFRFLDPFAKVVGDQGQCHSTDIVTKNLDPKXNQHYD 66  
 Db 8 RRNGTHKVRITILCARNLARDFLRPLDPFAKQVQDGTQGVYSTEISKSLDPKXNAHYD 67  
 Qy 67 LYIGKSDSFTISYWNHKKIKHEKOGAGFLGCVRLLSAINRLKDQFLICKLGQNND 126  
 Db 68 LFLGGCDATITWQRKHHK-GSGFLGCYTRAPMNIOSLKGAFQRLDGLKLSPDDE 125  
 Qy 127 TVRGAIVVLSQSRD-----IGFCGQVYDCSR-LFDNDLDPGWEEERRTAGRIQY 175  
 Db 126 LVGRGIIILSKGPSSGPNLAIVGSDTGPSEDDSSESLPQGWEERTDNGRVY 185  
 Qy 176 LNHHTRTTOWERPRP-----ASEYSSPQRPLSCFV----- 191  
 Db 246 HRSRDLSTVASDEERHSTEILSSVGKENTSPITPSATTPGKKTSSNSSSAGGRTLEQ 305  
 Qy 207 -----DNTPIST-----N----- 216  
 Db 306 RPTNEPATPSSTSASAVRLHSNDNHVXTPKHTQHNGHAPPSTPTPTGQONYNCNAQ 365  
 Qy 217 GAT----CGQSSDPLRAE----- 231

ULT 8  
 61120 standard; Protein; 1035 AA.  
 ABB61120; first entry

26-MAR-2002

3 66	GSTSGNGSGOAQPOSASANGWTQEDAAATTPSPTTSPDRHSOSPPIPNSPPASTVTPSA 4 25
232	- - - - - RVRSORHRHNTMSRTHLHTPP - - - - - 251
4 26	NGVTPSNANSTPAGSGGSSRSYTAATPGQRSSRQQGEBSSTRRSSGTRNGTS 4 85
252	- - - - - DLPEGYEORTQOGQYFLHTQTYSTWHDPR 283
4 86	GGGGCGGSGORYASAIAAAANOQAAARPLFLPLPGMERYTQQGQYFLHTQTYSTWHDPR 5 45
284	VPRDL- - SNINCEELGPLPGWEIRNTAATGRVYDPAHNRITQFTDPRLSANLHLVLRQ 3 41
546	IPRDSDTQCHLTLDAGPLBSGWEQRKTAAGRVEFDHNNTTQFTDPFLSGSLTQMIERRG 6 05
3 42 N	- - - - - QLKQQQQQVSI- - - - - CPDDTE 3 61
606	TVPPTSAAANGTAPPASATPATPSAAAAPQATPASNATPTITTTNPFRIVPDLPQ 6 65
362	CL- - - TBYPRKRLDVQKLKILCQELSQQCOPQOGHCRLEVSSEEIFEESYRCYDMKRPK 4 16
666	GLLEGADLLKYYRRLDVKGKRALRTELQTMQPGQHGCRLEVSNEEIFEESYRLIMMRRAK 7 25
417	DLWKRLMKIKPRGEEGBDYGGVAREWLYLISHEMINPYGLFOYSRDDIYTLOINPDSAVN 4 76
726	DMRKLVMVKPGEBGDYGGVAREWLHLISREMINPOTGLFQTSRDDIYTLOINPDSAVN 7 85
477	PEHLSYPHFVGRRGMMAVFGHYYDGGFTIPPFQQLIGKSITLDDMELYDPDOLHNLYWI 5 36
786	PDEHSYFH- - - - - PDEHSYFH- - - - - LLLNKPIITGIDEGYDGPDLHRSITWW 8 19
537	LENDTGVLDRHTCTEHNNAGEITQHELKGNGSITPVNBENKEVYVRLVUNWRFLRGTEA 5 96
820	LESNNSGIIESTPSTENNSGALVYHELKPGGASTPVTEENKEVYVLYNTRFRMGRGIEQ 8 79
597	QFLAQKGFGNENVIPDHLKTFDEKELELITIGLGRIDYNDWKVNTRLKHCTPDNSIVKWF 6 56
880	QFLAQKGFGELIPSHLRFPDERELVYIGGISSIDNDWRNTBLKCTNNTIVLWF 9 39
657	WKAVEFTDERRARLIQFTGSSRVPLOGFKALO- - GAAGPRLFTIH-QIDACTNNLPK 7 12
940	WQVVSYSSENMRLLQFVTGSSRVPLOGRALQGSTGAVPRLFTIHLTDVPTQNLPK 9 99
713	AHTCFNRIDIPPESEYKLUJTAETTCGFAYE 7 48
1000	AHTCFNRIDIPPEYQQLCDKLTOAVEETCGFAYE 1 035
JUL 9	
AAW13385	AAW13385 standard; Protein; 766 AA.
AAW13385;	
10-JUL-1997	(First entry)
Human protein ubiquitin ligase p52.	
Protein ubiquitin ligase; pub2; cdc25 phosphatase; CDK kinase; p53; cell cycle; transgenic animal.	
Homo sapiens.	
WO9712962-A1.	
10-APR-1997.	
04-OCT-1996;	96WO-US15930.
04-OCT-1995;	95US-0539205.
(COLD-) COLD SPRING HARBOR LAB.	

Page 10

586	VNRFLRGIEAQFLAQKGNEVTPQHLLKTFDKEELIICLGKDNDWKVNTRLKH	645
606	TW-1QKRIBEQAQNFAHEGSESELLPQEINVEDRELIGGISEIDMEWKHKDYS	664
646	CTPDNSITVKNEWKAVEFFDEERRARLQQFTGSSRVPLOQGXFTKALQAGPRIFTIHQIDA	705
665	YSENDOIIKRNWEMLADEWSNEKKRQLLQQTTSRIPINGFQDLQSGDPRKFTIEKAGE	724
706	CTNLPKAHTCFNRIDIPPYESYKLYEKILTTAETTCGFAVE	748
725	-PNKLPKAHTCFNRIDLPPYTSKQDLDHKLSIAVEETIGGQE	766
LT		
459	ABP73459 standard; Protein; 832 AA.	10
ABP73459;		
30-JAN-2003	(first entry)	
Candida albicans	essential protein	SEQ ID NO 7296.
Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;		
signal transduction; DNA replication; cell division; growth;		
proliferation; Candida albicans; fungicide; antifungal.		

WC00253728-A2.  
11-JUL-2002.  
26-DEC-2001; 2001WC-US49486.  
29-DEC-2000; 2000US-259128P.  
20-FEB-2001; 2001US-0792024.  
22-AUG-2001; 2001US-314050P.

(ELITR) ELITRA PHARM INC.  
Roemer T, Jiang B, Boone C, Bussey H, Ohlsén KL;  
WPI: 2002-566694/60.  
NPSSDB; AB22009.

Constructing strains for identifying gene products as effective targets for therapeutic intervention by inactivating one allele of a gene under control of a promoter and placing a second allele of the same gene under control of a different promoter.

expression -

The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement of a cassette having an expressible selectable marker and modifying other allele by recombination of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an anti-fungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identification of C. albicans cells and for ability to inhibit growth or proliferation of C. albicans cells and for

CC	treating infection by <i>C. albicans</i> . The present sequence is that of an essential <i>Candida albicans</i> protein used in the method of the invention.
CC	Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.
CC	
CC	
XX	
SQ	Sequence 832 AA;
Query Match	37.9%
Best Local Similarity	31.4%
Matches	338
Similarity	Conservative
Score	1530.5;
Pred. No.	5.7e-135;
Mismatches	120;
Indels	228;
Gaps	195;
Length	832;
	21;

6 FRRNGVVKRLTIVLCAKNLVKKDFRLLPDPFAKTVVDGSGQCHSTDYKNTLDBKANQH 65  
 9 RSNNNTTINYKVAEESLYKDRVQDFAVLTDG5-QTKTTITAKTKLNPNWNETF 67  
 66 DLYIGGSDSV-TISYWNHKLKHKOGAGFGCVR---LLSNAIRNLKDGTGWHORLCLK 119  
 120 LGPNNDTIVRGQIVVSLSCSRDRIGTGQVVD--- 150  
 124 -SNENLAWSKIIIVI-SHNRSNNGGVTITATRGASSNNIATITSGVNVLIGSA 160  
 151 -----  
 181 TTANTSTAQSADATVGANGSGPTSSLPPGQGHPEATAATPGGAGAGAAstroYSFED 240  
 158 ---DLDGWEBSRRTASGRICOLYLNHTTRTOWERPRPASE--- 194  
 241 QYGRLLPGWERTDNPGRTYVDRHNSRTTWQRPAHQSETERGQRQSETEARRQRHG 300  
 195 YSSPGR---PLSCFDENTPISTGNGATCGOSS---DPLRAERRVRSQRHRN 240  
 301 RTLPQGGSVSP---PTGSGSISNTVNTAASNANTPVPAAVMSMAASGATS 352  
 241 YMSRTHHTPDPDIBEGYEQRTTQGQVYELHTQGUSTWHDPRVPRDLSVN--- 292  
 353 GLG-----ELPSWEQRTETGPRPFYDVHNTTTWDPRRCQYIRTFGPNTIQQQ 404  
 293 -CEBLGLPGLPGWEIRNTATGRVYFDHANNRTTQFDRPLRSANLHLVLRNQNQLDKDQQQQ 351  
 405 PYSQLPGPSWEMRLNTNTARYVFBNNTKTTWDPRPSSL---DO---449  
 352 VVSLCPDDECLTVPRYKRDLYQKLKILRQLSQOPQ---AGHCRIEVSREEFEESY 407  
 450 -----NPVQYKDRFRKYVFR---SPALRILPQGOCHIKYRDRHIEDFSY 492  
 408 RQVNKRKPRKDLYKRLMKFRGEGLGQYGGVAREWLWLLSHMLNPVYGLQYSRDDIYTL 467  
 493 QEIMRQTPEDLKKRMLKFDGEGLQYGGVSEFFPLSHDMFNPFYCLPESSHDNYTL 552  
 468 QINPDSAVNPEHLSYPHVGRGMAGMVFHGHIYDGGFTLPPYKQLGKSFTLDDMELVDP 527  
 553 QINPNSGINPEHLYNKFEGRVVGLGYHFRFLDAFPVGALEYKOMLHKVVQLQDMEGVDA 612  
 528 DJHNSLWILENDITGVLDHTFCVHENAYGETIQLHELKPNQKSIPNEENKEYTLYVN 587  
 613 BFRSLKWLNDITGLDLTSAEBSFGTEVEVILPKGRDIETEENKEYTELITE 672  
 588 WRFIRGIBAQFLAQGFNEVIPQHILKTFDEKELELIICLIGKIDVNDVNTRLKHCT 647  
 673 WRISKRVEQKAFIDGENLNPQEVNVEDRELELLIGLAEICEDWKHDTDGYQ 732  
 648 PDSMVNFMWKAEEFDEERRARLQQTWGSSRVPLOGFKALOGAAGRFLTIHQIDACT 707  
 733 ENDQVQFWKCCINEWSEQKARLQLTTGTSRIPNGFKDLQGSGPRTIEKAGE-A 791  
 708 NNLPKAHTCFNRDIPPYSEYKLYKULTALETCFCAVE 748  
 792 NOLPKSNCENYDIPPYTYDSESKOCLTLLAVEETGFOE 832

Sequence	869 AA;	36.0%; Score 1453.5; DB 24; Length 869;	
JLT 11 6104 ABU26104 standard; Protein; 869 AA.			Query Match 36.0%; Pred. No. 1.2e-127; Mismatches 229; Indels 243; Gaps 21;
ABU26104; 16-APR-2003 (first entry)			Query 11 PVKLRU-TVLCAKNLYKKDFER-----LPDPFAKUVVDGGSOCH 4.8
Aspergillus fumigatus essential gene protein #762. Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response. Aspergillus fumigatus.	Db	15 PASSRUCRVIAADGJYKRDYFRKSYIALLVVRLITSGAFAAFPDPFAVATGGB-QTH 7.3	Db 15 PDKWNTLDPKMNQHDLIGKSDSVTISVNHHKKTKHKKOAGFLGVRLI-----100
WO200286090-A2.	Qy	49 STDIVNTNLDPKMNQHDLIGKSDSVTISVNHHKKTKHKKOAGFLGVRLI-----100	Db 74 TTSVKTILNPYWNMFDVRVNEDSILAQIDFDRKF-KKDDQGFLGVINVIGVIDDLQ 1.3.2
31-OCT-2002.	Db	101 -----SNAINPLK-----DTQYQRLDICKGPNNNDTPPGQIVHSI-----136	Qy 101 -----SNAINPLK-----DTQYQRLDICKGPNNNDTPPGQIVHSI-----136
23-APR-2002; 2002WO-US13142.	Qy	133 MCGDGESLPIRHSCVSRLTRLLETEMTRDJKK-SNDNLVHGKLINLSTNLST 1.9.0	Db 133 MCGDGESLPIRHSCVSRLTRLLETEMTRDJKK-SNDNLVHGKLINLSTNLST 1.9.0
23-APR-2001; 2001US-285697P. 27-APR-2001; 2001US-287056P. 05-JUN-2001; 2001US-293890P. 09-JUL-2001; 2001US-303899P. 31-AUG-2001; 2001US-311632P.	Db	137 -----OSDRDGTGCGCVVDS-----152	Qy 137 -----OSDRDGTGCGCVVDS-----152
(ELITA) ELITA PHARM INC.	Db	191 PNTNQANGLHRSHYQSSTSSGLYQAVPSSHPAASTAPVDPASNSPNLNPORVPSTTR 2.50	Db 191 PNTNQANGLHRSHYQSSTSSGLYQAVPSSHPAASTAPVDPASNSPNLNPORVPSTTR 2.50
Jiang B, Tishkoff D, Zamudio C, Broshkin AM, Hu W, Lemieux SM; WPI; 2003-093124/08.	Qy	153 -----RLPFDN----LPDWEERDTASGRQIYLNHITRITQ 1.8.4	Qy 153 -----RLPFDN----LPDWEERDTASGRQIYLNHITRITQ 1.8.4
New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer -	Db	251 PSSTAAPASAAGAAYNSHGSRTNLSSFSQDQLPAGWERREDNLGRTRYYDHNTTRTT 3.1.0	Db 251 PSSTAAPASAAGAAYNSHGSRTNLSSFSQDQLPAGWERREDNLGRTRYYDHNTTRTT 3.1.0
Disclosure; Page : 175pp; English.	Qy	185 WERPTPASEYSSSPRPLSCFVDENTPISGTNGATCQSSDPRLAERRRSRSHRTM-----24.2	Qy 185 WERPTPASEYSSSPRPLSCFVDENTPISGTNGATCQSSDPRLAERRRSRSHRTM-----24.2
311 W--TRPSSNNYNEHAQ-----	Db	311 W--TRPSSNNYNEHAQ-----RSQEANQLERRAHQSRMLP 3.4.4	Db 311 W--TRPSSNNYNEHAQ-----RSQEANQLERRAHQSRMLP 3.4.4
243 -----SPTHHLTIPP-----	Qy	243 -----DLPEGYEORTTOOCQVY 2.6.8	Qy 243 -----DLPEGYEORTTOOCQVY 2.6.8
345 EDRTGANSPLNPLESSQQAHTPPAGCSANAVSMATGATTAGTGELPPWEQRTTPSERY 4.0.4	Db	345 EDRTGANSPLNPLESSQQAHTPPAGCSANAVSMATGATTAGTGELPPWEQRTTPSERY 4.0.4	Db 345 EDRTGANSPLNPLESSQQAHTPPAGCSANAVSMATGATTAGTGELPPWEQRTTPSERY 4.0.4
269 FLHTQTGVSTWHDPVRPDL-----SNIN-----CEEGLGPLPPGWETNTATGRVY 3.1.4	Qy	269 FLHTQTGVSTWHDPVRPDL-----SNIN-----CEEGLGPLPPGWETNTATGRVY 3.1.4	Qy 269 FLHTQTGVSTWHDPVRPDL-----SNIN-----CEEGLGPLPPGWETNTATGRVY 3.1.4
405 FVDHNTTRTWWDPDPLPSS-----DQ-----	Db	405 FVDHNTTRTWWDPDPLPSS-----DQ-----GVQYKRDFRR 4.6.4	Db 405 FVDHNTTRTWWDPDPLPSS-----DQ-----GVQYKRDFRR 4.6.4
315 FVDHNTTRTQFTDPISANLHLVNRQNOLKDQQQQVYSLCDDETECLTVPRYKRDVLQ 3.7.4	Qy	315 FVDHNTTRTQFTDPISANLHLVNRQNOLKDQQQQVYSLCDDETECLTVPRYKRDVLQ 3.7.4	Qy 315 FVDHNTTRTQFTDPISANLHLVNRQNOLKDQQQQVYSLCDDETECLTVPRYKRDVLQ 3.7.4
465 FVDHNTTRTWWDPDPLPSS-----DQ-----	Db	465 FVDHNTTRTWWDPDPLPSS-----DQ-----GVQYKRDFRR 4.9.7	Db 465 FVDHNTTRTWWDPDPLPSS-----DQ-----GVQYKRDFRR 4.9.7
375 KLUKILQEELSQQP-----QAGHCRLEVSREEIFPESTYQVMQRPKDILWKRLMKIFKGEE 4.3.0	Qy	375 KLUKILQEELSQQP-----QAGHCRLEVSREEIFPESTYQVMQRPKDILWKRLMKIFKGEE 4.3.0	Qy 375 KLUKILQEELSQQP-----QAGHCRLEVSREEIFPESTYQVMQRPKDILWKRLMKIFKGEE 4.3.0
498 KLIYER-----SQPALRIMSQGHVYKVRNNNIFDSYAEIMROSAIDLKGRLMKIFGED 5.5.2	Db	498 KLIYER-----SQPALRIMSQGHVYKVRNNNIFDSYAEIMROSAIDLKGRLMKIFGED 5.5.2	Db 498 KLIYER-----SQPALRIMSQGHVYKVRNNNIFDSYAEIMROSAIDLKGRLMKIFGED 5.5.2
431 GLDYGGVAREWLYLISHEMLNPPYYGLFOYSRDDTYLQINPDSAVNPHELSYTFHVGRIM 4.9.0	Qy	431 GLDYGGVAREWLYLISHEMLNPPYYGLFOYSRDDTYLQINPDSAVNPHELSYTFHVGRIM 4.9.0	Qy 431 GLDYGGVAREWLYLISHEMLNPPYYGLFOYSRDDTYLQINPDSAVNPHELSYTFHVGRIM 4.9.0
553 GLDYGGLSGEFFPLSHEMNPFCOLFEPSAHNTYQINPHSGVNPHENYFKFISRVV 6.1.2	Db	553 GLDYGGLSGEFFPLSHEMNPFCOLFEPSAHNTYQINPHSGVNPHENYFKFISRVV 6.1.2	Db 553 GLDYGGLSGEFFPLSHEMNPFCOLFEPSAHNTYQINPHSGVNPHENYFKFISRVV 6.1.2
491 GMAVIGHYIDGGFLPPLYKOLIGKSITLDDMELVDPLHNSLWLLENDITGVLDHTFC 5.5.0	Qy	491 GMAVIGHYIDGGFLPPLYKOLIGKSITLDDMELVDPLHNSLWLLENDITGVLDHTFC 5.5.0	Qy 491 GMAVIGHYIDGGFLPPLYKOLIGKSITLDDMELVDPLHNSLWLLENDITGVLDHTFC 5.5.0
613 GIAIFERRFLDFFGAFYKMRMLRKVSLQDMBSEDELRHNTTWNDLLEGVLTSFS 6.7.2	Db	613 GIAIFERRFLDFFGAFYKMRMLRKVSLQDMBSEDELRHNTTWNDLLEGVLTSFS 6.7.2	Db 613 GIAIFERRFLDFFGAFYKMRMLRKVSLQDMBSEDELRHNTTWNDLLEGVLTSFS 6.7.2
551 VEHNAEGEIIQHKEPKNGKSIPVNEHENKEYRYVYNNPDRFGIEAQFLAQKGNEVIP 6.1.0	Qy	551 VEHNAEGEIIQHKEPKNGKSIPVNEHENKEYRYVYNNPDRFGIEAQFLAQKGNEVIP 6.1.0	Qy 551 VEHNAEGEIIQHKEPKNGKSIPVNEHENKEYRYVYNNPDRFGIEAQFLAQKGNEVIP 6.1.0
673 VDDEKEFERRTIDLPGGGRDIPVNTENKAEXYVLTENKVEOFNAFMGSFNLIP 7.3.2	Db	673 VDDEKEFERRTIDLPGGGRDIPVNTENKAEXYVLTENKVEOFNAFMGSFNLIP 7.3.2	Db 673 VDDEKEFERRTIDLPGGGRDIPVNTENKAEXYVLTENKVEOFNAFMGSFNLIP 7.3.2
611 QHLKTFDEKELELICLGKIDYDNWKNTNLKHTCDSNIVKWFKAVERFDEERRAR 6.7.0	Qy	611 QHLKTFDEKELELICLGKIDYDNWKNTNLKHTCDSNIVKWFKAVERFDEERRAR 6.7.0	Qy 611 QHLKTFDEKELELICLGKIDYDNWKNTNLKHTCDSNIVKWFKAVERFDEERRAR 6.7.0
733 ADLVNFYDERSELELIGGADIDVWDKXHTDGYQESDEVIQNFVKVRSWDAEOKSR 7.9.2	Db	733 ADLVNFYDERSELELIGGADIDVWDKXHTDGYQESDEVIQNFVKVRSWDAEOKSR 7.9.2	Db 733 ADLVNFYDERSELELIGGADIDVWDKXHTDGYQESDEVIQNFVKVRSWDAEOKSR 7.9.2
671 LLQFTGTSRVPLOQSKAALGAQGRPLFIHQ1DACTNINLPKAHTCNRIDAPPYESYEK 7.3.0	Qy	671 LLQFTGTSRVPLOQSKAALGAQGRPLFIHQ1DACTNINLPKAHTCNRIDAPPYESYEK 7.3.0	Qy 671 LLQFTGTSRVPLOQSKAALGAQGRPLFIHQ1DACTNINLPKAHTCNRIDAPPYESYEK 7.3.0
793 LIQFTGTSRVPLOQSKAALGAQGRPLFIHQ1DACTNINLPKAHTCNRIDAPPYESYEK 7.4.8	Db	793 LIQFTGTSRVPLOQSKAALGAQGRPLFIHQ1DACTNINLPKAHTCNRIDAPPYESYEK 7.4.8	Db 793 LIQFTGTSRVPLOQSKAALGAQGRPLFIHQ1DACTNINLPKAHTCNRIDAPPYESYEK 7.4.8
852 LEHKMSIAVEETLGQQE 8.6.9	Qy	852 LEHKMSIAVEETLGQQE 8.6.9	Qy 852 LEHKMSIAVEETLGQQE 8.6.9

RESULT 12

AAW93167  
XX  
AC  
AAW93167;  
XX  
AC  
AAW93167;  
XX  
DT  
24-MAY-1999 (First entry)

Human ZGGBP1 protein.		Qy 228 -----LABR-----RVRS-----	Db 328 SREELSRBLQTIPDSNQEQQSSLTQREPSRSVSCYTDVAEQHTPPPSVAYVETTPGL	Qy 253 QRHANMSRTHLHTPPDIL 253
ZGGBP1; bipolar affective disorder type I; human; neurological disorder; regulator; antisense; treatment; disease; stroke; dementia; renal; hypertension; nephrosis; cardiovascular.		Db 254 PEGYBORTTCGQGYFLHQTGTVSTWDP-----	Qy 254 RVPDRL 288	
Homo sapiens .		Db 388 PSGWEEERDKAGRTYYVHNHNRRTWTRPIMQLAEDGASGSATNSNNHLIBPQIQRSL	Qy 447 447	
Key Protein	Location/Qualifiers	Qy 289 SNINCEBLGP-----	Db 448 SSPTVTLXAPLEGAKDSPYRAVKDTLSPNQSPQPSPYNSPKPQHKTUQSFPGPBMRI	Qy 507 307
1..975	/label= ZGGBP1	Db 448 A2NGEPEFFIDENRTKTTWDPLRKPV-----	Db 448 A2NGEPEFFIDENRTKTTWDPLRKPV-----	Db 507 359
Misc-difference 455	/note= "Partial sequence"	Qy 308 TATGRRVYFVDHHNNTTOFTDPRLSANLHLVLRNQNOLKDQQQQVVSCLCPD-----	Db 508 RSKTSLNPNDLGPPGW	Db 554 554
WO9906539-A1.		Qy 360 -----TECHTVPR--YKRDLVQKIKLILQELSQQQPQ	Db 555 EERIHLDGRTFYIDINSKITQWEDPRLONPAITGPAYSVRFQKQDYFRCKLKRPADI	Qy 389 614
11-FEB-1999.		Db 615 PNRFEWKLHRNNIFFESYRIMSYKRDPLKARLWIESEKGLDQCGVAREWLYLISHE	Qy 615 PNRFEWKLHRNNIFFESYRIMSYKRDPLKARLWIESEKGLDQCGVAREWLYLISHE	Qy 448 448
28-JUL-1998;	98HO-GB02259.	Db 735 FYKMMGKQITLNDNSVDEYYNSKLWILENDPT-ELDLMPCIDEENFGTYQVDIKPN	Db 735 FYKMMGKQITLNDNSVDEYYNSKLWILENDPT-ELDLMPCIDEENFGTYQVDIKPN	Db 674 674
(ZENE ) ZENECA LTD.		Qy 736 PYKOLIGKSITLDDMELVDEPLIANSWVILENDTGVDLDTHTFCVHENAYGETIQHEIKPN	Db 736 PYKOLIGKSITLDDMELVDEPLIANSWVILENDTGVDLDTHTFCVHENAYGETIQHEIKPN	Db 567 567
Finnegan MCM,	Flannery AV;	Db 736 FGERMNTNENERYDLVQWRFVRVQRMNAFLBGPFLPIDLKIFDNELLLMC	Db 736 FGERMNTNENERYDLVQWRFVRVQRMNAFLBGPFLPIDLKIFDNELLLMC	Db 793 793
WPI: 1999-1153769/13.		Qy 794 GKS1PNEENKKEYVRLYNNWRFLRGIAQFLAQGFNEVIFQHLIKTDEKELELLIC	Db 794 GSEIMTNENREYDLVQWRFVRVQRMNAFLBGPFLPIDLKIFDNELLLMC	Db 853 853
N-PSDB; AAX22554.		Db 854 GLGKIDYNDMKVNTLTK--HCTPDSNIYVWFMKAVEFFDEERARLICFGTCSRPLQG	Db 854 GLGKIDYNDMKVNTLTK--HCTPDSNIYVWFMKAVEFFDEERARLICFGTCSRPLQG	Db 854 854
New isolated gene associated with neurological disorders - used to develop products for treating e.g. stroke, dementia, renal disorders, hypertension or cardiovascular disorders		Qy 854 GLGKIDYNDMKVNTLTK--HCTPDSNIYVWFMKAVEFFDEERARLICFGTCSRPLQG	Db 854 GLGKIDYNDMKVNTLTK--HCTPDSNIYVWFMKAVEFFDEERARLICFGTCSRPLQG	Db 912 912
Claim 1; Page 42-46; 58pp; English.		Db 912 FKALQGAAGPPLPHTQIDACTNNLPKAHTCFCNIDIPPYSEYKLYEKLTIAEIICGF	Db 912 FKALQGAAGPPLPHTQIDACTNNLPKAHTCFCNIDIPPYSEYKLYEKLTIAEIICGF	Db 745 745
This sequence represents a human ZGGBP1 protein which is associated with affective neurological disorders such as bipolar affective disorder type I. The invention also describes the isolation of the corresponding mouse genes. The ZGGBP1 protein and homologues or fragments of the protein which selectively bind to it and in so doing regulate the activity of the protein. The antisense DNA or antisense RNA may be of use in the treatment of diseases or disorders in humans in which the over- or under-regulated production of the gene product has been implicated, e.g. neurologic (stroke, dementia), renal (hypertension, nephrosis), cardiovascular disorders.		Db 912 FKALQGAAGPPLPHTQIDACTNNLPKAHTCFCNIDIPPYSEYKLYEKLTIAEIICGF	Db 912 FKALQGAAGPPLPHTQIDACTNNLPKAHTCFCNIDIPPYSEYKLYEKLTIAEIICGF	Db 971 971
Sequence 975 AA;		RESULT 13		
JERI Match 34.3%; Score 1387; DB 20; Length 975;		AAW36797 standard; Peptide; 724 AA.		
1st Local Similarity 31.4%; Pred. No. 2.0e-122; Mismatches 247; Indels 258; Gaps 26; matches 330; Conservative		XX ID AAW36797		
14 LRLTVICAKNLVKQDFRLDPFAKV--VVPGSSGQCH--STDIVKNTLDPKXNQHYDLY 68		AC AAW36797;		
42 LRVKTVSGIDLAKDFGASDPYTKLSSLVYADNRELAVQTKTKTLLNKWNBEFYFR 101		XX DT 23-APR-1998 (first entry)		
69 IGKSD-SVTISVWNHKIRKQGAGFLGCVR-----LUSNAIN 105		XX Novel human gene, designated WWP4.		
102 VNPNSNRLLFVFDENRLTRDD--FLGQDVPLSHLPLTEDTMERYTFXDFLLRSH 156		XX XX		
106 RLKDQYQLDLCKGPNNDTIVRQGVVSLQERDRIGCTGGVDCSRLFOND-----158		XX PEPTIDE RECOGNITION UNIT; YAP WW DOMAIN BINDING PROTEIN; WBP-1; WBP-2;		
159 ----LPDGWEERETASGRIOYLNHITRTTOWERPT-----189		XX KW Peptide recognition unit; YAP WW domain binding protein; WBP-1; WBP-2;		
209 BLPPPLPPLPPGEEKYDNLGRTYVNNHNRNTWHRPSMDVSESDDNIRQINQEAAHRR 268		XX KW Peptide recognition unit; YAP WW domain binding protein; WBP-1; WBP-2;		
190 ---RDAEYKSSP-----GRFLSCFVDFNPISGN-----GATGQSSDPR-- 227		XX KW Peptide recognition unit; YAP WW domain binding protein; WBP-1; WBP-2;		
269 FRSRHIISELEPEPEPEGDVPEPWET-TSEEVNAGDSLGVVLPPPPASGSRSPQEL 327		XX KW Peptide recognition unit; YAP WW domain binding protein; WBP-1; WBP-2;		
		Key misc_difference 1..3		
		/note= "the nucleotides encoding these amino acids are not given in the specification"		
		FT FT Domain		140..165 /note= "claimed (claim 49) WW Domain 1"
		PH FT Domain		252..277 /note= "claimed (claim 49) WW domain 3"
		FT FT Domain		303..328 /note= "claimed (claim 49) WW domain 3"
		FT FT Domain		618..724 /note= "claimed (claim 49) HECT domain"
		FT FT		/note= "claimed (claim 90) HECT domain"



Disclosure; Page 68-71; 79pp; English.

This invention describes a novel assay identifying an inhibitor of ubiquitin-mediated proteolysis of a IkappaB polypeptide. The method comprises: (a) providing a ubiquitin-conjugating system including the IkappaB polypeptide and a HECT (Homologous to EG-AP Carboxyl Terminus) ligase and ubiquitin, to promote ubiquitination of the IkappaB polypeptide by the HECT ligase; (b) contacting the ubiquitin-conjugating system with a candidate agent; (c) measuring a level of ubiquitination of the polypeptide in the presence of the candidate agent and (d) comparing the measured level of ubiquitination in the presence of the candidate agent with ubiquitination of the IkappaB polypeptide in the absence of the candidate agent, where a statistically significant decrease in ubiquitination of the IkappaB polypeptide in the presence of the candidate agent is indicative of an inhibitor of ubiquitination of the IkappaB polypeptide. The assays can be used to identify compounds which modulate binding and/or ubiquitylation of an IkappaB (or other cellular or viral substrate) by a HECT ligase, such as RSC or KIAN. Such modulators can be used e.g. in the treatment of proliferative and/or differentiative disorders, to modulate apoptosis, in the treatment of viral infections, and/or in the treatment of tissue wasting disorders e.g. cachexia secondary to infection or malignancy, cachexia secondary to human AIDS, inflammatory diseases, parasitic diseases, tuberculosis and high dose IL-2 therapy; rheumatoid arthritis, spondylitis, osteoarthritis, gouty arthritis and other arthritic conditions, sepsis, respiratory distress syndrome, cerebral malaria, chronic pulmonary inflammatory disease, silicosis, pulmonary sarcoidosis, bone resorption diseases, reperfusion injury, graft versus host reaction, allograft rejections, Crohn's disease, ulcerative colitis, or pyrexia, in addition to a number of autoimmune diseases such as multiple sclerosis, autoimmune diabetes, systemic lupus erythematosus; and ENL in leprosy, HIV, and AIDS. This sequence represents a human KIAN ligase which is used in the method of the invention.

Sequence 927 AA:

try Match	33.5%	Score 1354.5;	DB 20;	Length 927;		RESULT 15
st Local Similarity	34.0%	Pred. No. 3e-11.8;				AAE32725
tches	329;	Conservative 123;	Mismatches 232;	Indels 285;	Gaps 28;	ID AAE32725 standard; Protein: 927 AA.
						XX
4 PGERRNGRV-----		KLRITVLCAKNVKKDFFPFLDPAK 38				AC
13 PGFRGRAVCWRSEMA	TCAYEVFGLEDEENSRIVRVIAGLAKKDDILGASDPPV 72					XX
39 VV--YTDGSQGOCHSTTVNTLDPKNN-----OH-----YDLYGK 71						DT 24-MAR-2003 (first entry)
73 VTDVDPNGVLSVQRTIKKSINPKNEELFRVHPQERLLEPFDENRLPRDDFJGQ 132						XX
72 SD--SVTISVWN-----HKKTHKKKGAGGFLGCVRLLSNAINRLLDTGYQL 115						DB Human NEDD4 long form protein.
133 VDVPLVPLPTENPLERPYTFKDVFVLPKRSKSRVGYL-----RLKMT-----176						XX
116 DICKLGPNNDTDTYRGQIVVSQSRDRGTGQVVD----C-----SRLFDNDLFDGWEERR 167						KW Viral infection; lymphosarcoma; human immunodeficiency virus; hepatitis; HIV; measles; protein therapy; human; NEDD4.
177 YLPKTSGSDD-----NAQAEELPEGMVNLQDPAACLQQQEPSPPLPPGWEERQ 228						XX
168 TASGRIQYLNHTTTQERT-----RPASE-----194						OS Homo sapiens.
229 DILGRTYYTNHESRRTQKRTPIDQNLTAENGNIQIAQRAFTRRQISEETESVDOQE 288						XX
195 -----YSS--PGRLPLSCFEDNTPLSGT-----C-----SRLFDNDLFDGWEERR 227						FT Key Domain 381..406
177 YLPKTSGSDD-----NAQAEELPEGMVNLQDPAACLQQQEPSPPLPPGWEERQ 228						FT /note= "WW domain"
289 SSENTEBIREDEATMYSQAFFSSPPSSNLDVPTHLAELNARTIGNSAVSQPASSNN 348						XX 82..923 "HECT domain"
228 LAER-----VSRQRERNTM---SRTHLHTPD-----NGATCCQSSDR 252						FT /note= "HECT domain"
349 HSRRGGSLQAYTFFEEQPTLPVLLPTSSGLPPGWEERQDERSYVHDNSRTTWKPIV 408						XX (PROT-) PROTEOLOGICS LTD.
253 -----LPEGYEORITQOOGQVYFLH 271						XX PI Greener T, Moskowitz H, Reiss Y, Alroy I;
409 QATVETSIQUTSSQQSAGPQSACSTSDDQQVTQPSSEEQGFLPKGEWEIRNTATGRVYFYDHNRR 321						DR WPI; 2003-111976/10.
272 TQTGVSTWHDR--VPR-----DLSNINCEBLGPPLPPGWEIRNTATGRVYFYDHNRR 321						DR N-PSDB; AAD50459.

Sequence	927 AA;	try Match	33.5%	Score	1354.5;	DB	24;	Length	927;
		Local Similarity	34.0%	Prod. No.	3e-1118;				
		t Local Similarity	34.0%	Minmatch	222;	Trend	205;	Gaps	26
		Conservear	122;						
		ches 320.							

229 DILGRTTYVNHESRTOQKRPTQDNLNTDAENGNIQIQAQRATFRROISSETETSYDNQE 288  
195 -----YSS-----PGRPLSCFVDENTPISGT-----NGATGQSSDPR 227

289	SSENWEILREDEATMYSSQAFPSPPPSNNLDVPTHLAELLNARLTIFGNSAVSQASSSN	348
228	LAEER-----	252
349	HSSRSHSLOYATTPEOCTPLVILPTSSGPPWEXEOKDERGSYVDDNSRTTTWKPTV	408
	-----VRSQRHRYNM-----SPTHLHPPD-----	

253 -----LPEGEORTTOGGQYFLH 271

272 TQGVSTWDPR--VPR-----DLSNINCEELGPLPPGWEIRNTATGRVYFVDHNNR 321

469 HNIKLTWEDPLKIPAHLRGKSLDTSN---DLGPPLPGWBERTHDGRIFTINHNT 524  
322 TTQFTDPRLSANLHLVNRQNLKDQQQQVSYCLCPDTECLTYPR-YKDRDLYOKLKIL 379

439	REWILLYLHEMINPPYYGLFOYSRSDDTIQLQINPDSAV-NPEHLSYFFVGRIMGMVAFHG 497	
617	REWFLISKEMENPPYYGLFEYSAITDNTVNLQINPNSGCLNEDHLSYFFVGRAGMAYFHG 676	
498	HYTDGGFTLPFYQOLIGKSIITDDEMVYDPLIHSWILENDITGYLDHTFCEVHNAYG 557	
677	KLLDGFIFRPFYKMLKPIIHDMSEVSDTSEYNSLWILENDPT-ELDLRFIDELFLG 735	
558	EIIQHELKPGKSTIPVNENKKKEYVRLYVNNWRFLRGIEAQFLALQKGSENEVIFQHLKTF 617	
736	QTHQHELKNGGSEIVVTNKNCKEIVYLVQWFVNRIQKONAAFKEGFFELIQDLKIF 795	
618	DEREBLELITLGKIDNDWKUNTRLKH-CTPDSNIYFNWKAWEFDEERARLQFVT 676	
796	DENELELMCGLGVDNDWRELTHTKYNGGSANHQVQWFMWKAVALMMDSEKIRLQFVT 855	
677	GSSRVPLQCFKALQGAAGRLFTIHQDACTNPNLPAHTCFCRIDPYYESVEKLYEJL 736	
856	GTSEVRVPNGFABLYGSNSPQSFTIVEQW-GTPERKLPRAHTCFNRDLIIPYESFBEULDKLQ 914	
737	TATIREBTCTGP 745	

Search completed: February 20, 2004, 15:28:33  
Time : 45.6968 secs

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protein - protein search, using sw model

n on: February 20, 2004, 15:26:11 ; Search time 15.7634 Seconds  
(without alignments)

title: US-10-009-945-4  
refect score: 408

quence: 1 NSNPGRRRNGEVKRLTVLC.....EKLYEKLLTAIEETCGPAVE 748

oring table: Gapop 10.0 , Gapext 0.5

arched: 328717 seqs, 42310858 residues

tal number of hits satisfying chosen parameters:

328717

minimum DB seq length: 0  
maximum DB seq length: 2000000000

st-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

atabase : Issued Patents AA:  
1: /cgn2\_6\_ptodata/1/iaaa/5A\_COMB.pep:  
2: /cgn2\_6\_ptodata/1/iaaa/5B\_COMB.pep:  
3: /cgn2\_6\_ptodata/1/iaaa/6A\_COMB.pep:  
4: /cgn2\_6\_ptodata/1/iaaa/6B\_COMB.pep:  
5: /cgn2\_6\_ptodata/1/iaaa/PCTUS\_Comb.pep:  
6: /cgn2\_6\_ptodata/1/iaaa/backfile1.pep:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

built No.	Score	Query	Match %	Length	DB ID	Description
1	3939.5	97.6	735	3	US-08-539-205A-2	Sequence 2, Appli
2	3939.5	97.6	735	4	US-08-539-162A-2	Sequence 2, Appli
3	1564	38.7	766	3	US-08-539-205A-4	Sequence 4, Appli
4	1564	38.7	766	4	US-09-392-162A-4	Sequence 4, Appli
5	1354	33.5	927	3	US-08-895-601-6	Sequence 6, Appli
6	1353	33.5	834	3	US-08-539-205A-6	Sequence 6, Appli
7	1353	33.5	834	4	US-09-392-162A-6	Sequence 6, Appli
8	1336	33.1	854	2	US-09-070-060-4	Sequence 4, Appli
9	1336	33.1	854	3	US-09-357-746-4	Sequence 4, Appli
10	1329	32.9	852	2	US-09-070-060-3	Sequence 3, Appli
11	1329	32.9	852	3	US-09-357-746-3	Sequence 3, Appli
12	1298.5	32.2	906	3	US-08-630-912A-48	Sequence 4, Appli
13	1134.5	28.1	683	3	US-08-630-912A-46	Sequence 4, Appli
14	534.5	13.2	874	2	US-08-247-904B-8	Sequence 2, Appli
15	534.5	13.2	874	3	US-08-767-942A-21	Sequence 2, Appli
16	513	12.7	866	1	US-08-100-692-1	Sequence 1, Appli
17	513	12.7	866	2	US-08-674-030-1	Sequence 1, Appli
18	450.5	11.2	1083	3	US-08-895-601-5	Sequence 5, Appli
19	219	5.4	486	3	US-08-341-510C-2	Sequence 2, Appli
20	207	5.1	472	3	US-08-338-518C-5	Sequence 5, Appli
21	207	5.1	472	3	US-08-476-509B-5	Sequence 5, Appli
22	162.5	4.0	54	3	US-08-630-912A-124	Sequence 124, Appli
23	158	3.9	448	3	US-08-505B-2	Sequence 2, Appli
24	156.5	3.9	55	3	US-08-630-912A-75	Sequence 75, Appli
25	154.5	3.8	454	3	US-08-348-518C-4	Sequence 4, Appli
26	154.5	3.8	454	3	US-08-476-509B-4	Sequence 4, Appli
27	153	3.8	224	3	US-08-630-912A-50	Sequence 50, Appli

28	150	3.7	51	3	US-08-630-916A-117	Sequence 117, App
29	147.5	3.7	54	3	US-08-630-916A-74	Sequence 74, App
30	146	3.6	51	3	US-08-630-916A-73	Sequence 73, App
31	145.5	3.6	58	3	US-08-630-916A-84	Sequence 84, App
32	141	3.5	54	3	US-08-630-916A-118	Sequence 118, App
33	140	3.5	38	3	US-08-630-916A-26	Sequence 26, App
34	140	3.5	38	3	US-08-348-518C-19	Sequence 18, App
35	140	3.5	38	3	US-08-476-509B-18	Sequence 18, App
36	136	3.4	38	3	US-08-630-916A-36	Sequence 36, App
37	135	3.3	51	3	US-08-630-916A-116	Sequence 116, App
38	132	3.3	38	3	US-08-630-916A-32	Sequence 32, App
39	129.5	3.2	1105	4	US-09-720-517A-2	Sequence 2, Appli
40	129.5	3.2	335	51	US-08-476-509B-15	Sequence 2, Appli
41	127	3.1	38	3	US-08-630-916A-115	Sequence 15, App
42	127	3.1	38	3	US-08-348-518C-15	Sequence 15, App
43	124	3.1	38	3	US-08-630-916A-24	Sequence 24, App
44	124	3.1	38	3	US-08-476-509B-15	Sequence 15, App
45	124	3.1	38	3	US-08-476-509B-15	Sequence 15, App

#### ALIGNMENTS

RESULT 1									
US-08-539-205A-2									
; Sequence 2, Application US/08539205A									
; Patent No. 6004619									
; GENERAL INFORMATION:									
; APPLICANT: Beach, David H.									
; APPLICANT: Caliguri, Maureen									
; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto									
; NUMBER OF SEQUENCES: 6									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEEE: FOLEY, HOAG & ELIOT LLP									
; STREET: One Post Office Square									
; CITY: Boston									
; STATE: MA									
; COUNTRY: USA									
; ZIP: 02109-2170									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
; COMPUTER: IBM PC compatible DOS									
; OPERATING SYSTEM: PC-DOS/MS-DOS									
; SOFTWARE: Patent In Release #1.0, Version #1.30									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/08/539-205A									
; FILING DATE: 04-OCT-1995									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Vincent, Matthew P.									
; REGISTRATION NUMBER: 36,709									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: (617) 832-1000									
; TELEFAX: (617) 832-7000									
; INFORMATION FOR SEQ ID NO: 2:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 735 amino acids									
; TYPE: amino acid									
; TOPOLOGY: linear									
; MOLECULE TYPE: protein									
; US-08-539-205A-2									
; Query Match 97.6%; Score 3939.5; DB 3; Length 735;									
; Best Local Similarity 98.0%; Pred. No. 0; Mismatches 0; Indels 13; Gaps 1;									
; Matches 733; Conservative 0;									
Qy	1	MSNPGRRRNGPVKRLTVLCKNLVKKDFFRFLPDPFPKTYKNTLDPK	60						
Db	1	MSNPGRRRNGPVKRLT-----GLPDPFPKTYKNTLDPK	47						
Qy	61	WNQHYDLYIGKSDSVTISYNNHKHHKKGAGFGLGVRLSNAIRLKDGYQLDCKL	120						

48 WNHYDLYIGKSDSVTISWNHKKHHQAGFLGCVRLLSNAINRLKDTGQRDLCKL 107  
 121 GRNDTTRGQIVNLSQSDRGTCQWDCSRFLPNDLPGWEERTASERIQLNHIT 180  
 108 GPNDDTTRGQIVNLSQSDRGCGVDCSRFLPNDLPGWEERTASERIQLNHIT 167  
 181 RTTOWERPRPASWSSPRPLSCFVDNTPIGTNGATCGOSSPDRLAEPVRQRHRN 240  
 168 RTTOWERPRPASWSSPRPLSCFVDNTPIGTNGATCGOSSPDRLAEPVRQRHRN 227  
 241 YMSRTHLHPPDLDGYEBORTTOOGTYFLHTGYSTWDPRPFDLSNINCEBGLPL 300  
 228 YMSRTHLHPPDLDGYEBORTTOOGTYFLHTGYSTWDPRPFDLSNINCEBGLPL 287  
 301 PGWEIRNTATGRYFVDINRITQFDERLSANLHLVLRNQLKQQQQCVSLCPDT 360  
 288 PGWEIRNTATGRYFVDINRITQFDERLSANLHLVLRNQLKQQQQCVSLCPDT 347  
 361 ECLTPRYKRDLVQLKLRQELSQOOQAGHCRIEVSREELFESEYRQWKMKPDKLK 420  
 348 ECLTPRYKRDLVQLKLRQELSQOOQAGHCRIEVSREELFESEYRQWKMKPDKLK 407  
 421 RLMXFRGRGEGDYGVAEMYLHSHEMLNYYGLFOYSRDDITYLQINPDSAVNPEHL 480  
 408 RLMXFRGRGEGDYGVAEMYLHSHEMLNYYGLFOYSRDDITYLQINPDSAVNPEHL 467  
 481 SYFHVGGRIMGMAYPHGYIDGAFTLPKYKOLGKSTLDDMELVDPDENSLYWILEND 540  
 468 SYFHVGGRIMGMAYPHGYIDGAFTLPKYKOLGKSTLDDMELVDPDHNLSLYWILEND 527  
 541 ITGVLDHHTPCVEINAYPELQHELPKNGKSIPVNENKEVRLTVNWRPLGEAQFLA 600  
 528 ITGVLDHHTPCVEINAYPELQHELPKNGKSIPVNENKEVRLTVNWRPLGEAQFLA 587  
 601 LQKGNEVTPHILKTDFEKELELICLGKIDDNWKVNTRLKHTCPDSNIVKMFVKAV 660  
 588 LQKGNEVTPHILKTDFEKELELICLGKIDDNWKVNTRLKHTCPDSNIVKMFVKAV 647  
 661 EFPDEERRARLQFTGSSRVPLQFGKALOGAAGRPLFTIHQIDACTNNLPKAHTCFNRI 720  
 648 EFPDEERRARLQFTGSSRVPLQFGKALOGAAGRPLFTIHQIDACTNNLPKAHTCFNRI 707  
 721 DIPPESYEKLYKLTAIEETCGFAVE 748  
 708 DIPPESYEKLYKLTAIEETCGFAVE 735

JUL 2  
 09-392-163A-2  
 sequence 2 Application US/09392163A  
 GENERAL INFORMATION:  
 APPLICANT: Beach, David H.  
 APPLICANT: Caliguri, Maureen  
 APPLICANT: Neftsky, Bradley  
 TITLE: Ubinquitin Ligases, and Uses Related Thereto  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109-2170

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/392,163A  
 FILING DATE:  
 PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 09/392,163A-2  
 FILING DATE: US 08/539,205  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Vincent, Matthew P.  
 REGISTRATION NUMBER: 36,709  
 PREFERENCE/DOCKET NUMBER: CSV-005.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 832-1000  
 TELEFAX: (617) 832-7000  
 INFORMATION FOR SEQ ID NO: 2;  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 735 amino acids  
 TYPE: amino acid  
 TOPOLOGY: 1-linear  
 MOLECULE TYPE: Protein  
 US-09-392-163A-2

Query	Match	Score	Length
Qy	97.6%; Best Local Similarity 98.0%; Matches 733; Conservative 0;	3919.5;	DB 4;
Db	1 MSNPGRNRGRRNRPVCKRLTIVLCAKNLVKKOFFRLDPFAKVYDVGSGQCHSTDYTKNTLDPK 60 1 MSNPGRNRGRRNRPVCKRLT-----GLDPFAKVYDVGSGQCHSTDYTKNTLDPK 47	0;	Mismatches 2;
Qy	61 WNOHYDLYIGKSDSUTISTWNHKHHQAGPGLGCVRLSNAINRLKDTGQRDLCKL 120 61 WNOHYDLYIGKSDSUTISTWNHKHHQAGPGLGCVRLSNAINRLKDTGQRDLCKL 107	13;	Indels 13;
Db	48 WNOHYDLYIGKSDSUTISTWNHKHHQAGPGLGCVRLSNAINRLKDTGQRDLCKL 107	1;	Gaps 1;
Qy	121 GPNDNDTVPQIVVLSQSDRIGGQVUDCSFLNDLPGDEBERTASGRQYQINHIT 180 108 GPNDNDTVPQIVVLSQSDRIGGQVUDCSFLNDLPGMEBERTASGRQYQINHIT 167	1;	
Qy	181 RTTOWERPTPASSEYSSPERPLSFVDENTPTSGTNGATCGOSSDPLAEPRVRSQRHNR 240 168 RTTOWERPTPASSEYSSPERPLSFVDENTPTSGTNGATCGOSSDPLAEPRVRSQRHNR 227	1;	
Qy	241 YMSTRHLHTPDPLPEGYORTTQGQYFLHTQGYSTWHDPRPFDLSNINCEBGLPL 300 228 YMSTRHLHTPDPLPEGYORTTQGQVFLHTQGYSTWHDPRPFDLSNINCEBGLPL 287	1;	
Db	301 PGWEIRNTATGRYFVDHHTPCVEINAYPELQHELPKNGKSIPVNENKEVRLTVNWRPLGEAQFLA 600 288 PGWEIRNTATGRYFVDHHTPCVEINAYPELQHELPKNGKSIPVNENKEVRLTVNWRPLGEAQFLA 587	1;	
Qy	361 ECUTPRYKTDIVQLKILQELSSQQQQQAGCIEYSGREEPEESTRQMKRPRDLWK 420 348 ECUTPRYKTDIVQLKILQELSSQQQQQAGCIEYSGREEPEESTRQMKRPRDLWK 407	1;	
Qy	421 RLMIIFRGERGEGDYGQVAREWLHSHMLNYYGLFOYSRDIYLTQINDSAVNEHL 480 408 RLMIIFRGERGEGDYGQVAREWLHSHMLNYYGLFOYSRDIYLTQINDSAVNEHL 467	1;	
Qy	481 SYFHVGGRIMGMAYPHGYIDGFTLPKYKOLGKSTLDDMELVDPDHNLSLYWILEND 540 468 SYFHVGGRIMGMAYPHGYIDGFTLPKYKOLGKSTLDDMELVDPDHNLSLYWILEND 527	1;	
Qy	541 ITGVLDTFCVERNAYGETQHELPKNGKSIPVNENKEVRLTVNWRPLGEAQFLA 600 528 ITGVLDTFCVERNAYGETQHELPKNGKSIPVNENKEVRLTVNWRPLGEAQFLA 587	1;	
Qy	601 LQKGFNEVTPQHLLKPKNSKIPVNENKEVRLTVNWRPLGEAQFLA 600 588 LQKGFNEVTPQHLLKPKNSKIPVNENKEVRLTVNWRPLGEAQFLA 587	1;	
Qy	661 EFPDEERRARLQVTGSSRVPLQFGKALOGAAGRPLFTIHQIDACTNNLPKAHTCFNRI 720 648 EFPDEERRARLQVTGSSRVPLQFGKALOGAAGRPLFTIHQIDACTNNLPKAHTCFNRI 707	1;	
Db	721 DIPPESYEKLYKLTAIEETCGFAVE 748 708 DIPPESYEKLYKLTAIEETCGFAVE 735	1;	

Query Match      38.7%; Score 1564; DB 3; Length 766;  
 Best Local Similarity 41.1%; Pred. No. 7.9e-138;  
 Matches 33B; Conservative 12I; Mis matches 232; Indels 132; Gaps 18;

SEQUENCE CHARACTERISTICS:  
 LENGTH: 766 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 -08-539-205A-4

Query Match      38.7%; Score 1564; DB 3; Length 766;  
 Best Local Similarity 41.1%; Pred. No. 7.9e-138;  
 Matches 33B; Conservative 12I; Mis matches 232; Indels 132; Gaps 18;

SEQUENCE CHARACTERISTICS:  
 LENGTH: 766 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 -08-539-205A-4

Query Match      38.7%; Score 1564; DB 3; Length 766;  
 Best Local Similarity 41.1%; Pred. No. 7.9e-138;  
 Matches 33B; Conservative 12I; Mis matches 232; Indels 132; Gaps 18;

SEQUENCE CHARACTERISTICS:  
 LENGTH: 766 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 -08-539-205A-4

Query Match      38.7%; Score 1564; DB 4; Length 766;

RESULT 4  
 US-10-009-945-4  
 ; Sequence 4, Application US/09392163A  
 ; Patent No. 650742  
 GENERAL INFORMATION:  
 APPLICANT: Beach, David H.  
 APPLICANT: Caliguri, Maureen  
 APPLICANT: Nefsky, Bradley  
 TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109-2170  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.1, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/539.205A  
 FILING DATE: 04-OCT-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Vincent, Matthew P.  
 REGISTRATION NUMBER: 36,709  
 REFERENCE/DOCKET NUMBER: CSV-005.01  
 TELECOMMUNICATION: (617) 832-1000  
 TELEPHONE: (617) 832-7000  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 766 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 -08-539-205A-4

Query Match      38.7%; Score 1564; DB 3; Length 766;  
 Best Local Similarity 41.1%; Pred. No. 7.9e-138;  
 Matches 33B; Conservative 12I; Mis matches 232; Indels 132; Gaps 18;

SEQUENCE CHARACTERISTICS:  
 LENGTH: 766 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 -08-539-205A-4

Query Match      38.7%; Score 1564; DB 3; Length 766;  
 Best Local Similarity 41.1%; Pred. No. 7.9e-138;  
 Matches 33B; Conservative 12I; Mis matches 232; Indels 132; Gaps 18;

SEQUENCE CHARACTERISTICS:  
 LENGTH: 766 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 -08-539-205A-4

Query Match      38.7%; Score 1564; DB 4; Length 766;

Best Local Similarity 41.1%; Pred. No. 7.9e-138; Matches 338; Conservative 121; Mismatches 232; Index 132; Gaps 18;

1 MSNPGRRNPGPPVQLRLTVLCAKNUKKDFERLDPFAKVVHDGSGQHSTDIVKNTLDPK 60  
 1 MSNSQSR ---RTRVTTAAGDGYKRDVERFDPAFLTVDGE-QTHTTTAIKTLNRY 55

61 WNHQHDLIGKSDSVTISWNHKKIHKGAGFLGCYRLLSNAINLKDTAYQL-DLC 118  
 56 WNETEVNVNDNSTAIIQFDQKPK-KKKGQFLGVINLRVGDVLDIAIGDEMILRDLK 114

119 KLGPNNDTIVRGIVVSLQ----- 137

115 K-SNEINTVHGKTIINLSTAOSTLQVPSAASGARTQRTSITNDPQSSKSSVSRNPA 172

138 -----SRDRTGCVYVDCSRLFDN-----DLPGWERRTAGRGIQYLNHTRTQ 184  
 173 SRSASPTRNAPASPASEPRFSSPPFDQYGRPLPOWERDNDGRTYVDDNTSRSTT 232

185 WERPT-----RPASEYSSPGRPLSCFIDENTPIGSTNGATCGQSSDPRLAERRYSQRH 238  
 233 WIRPLISSYAGAAAEELHSAS--SANTEGVQPSNSAA-----RTEASVLT--- 279

239 RNYMSRTHLHTPPDLPPEGYEQRTQOGQYFLHTQGIVSTWDHPYRVDLSGNIN---- 292

280 -----SNATPGSGLPPGMWQRVTPGRPFYDHENTTRTWYDPRQQYIERSYGGPNNA 335

293 -----CEREGPLPQWEIRNTATGRVYFDHNRTOQDPRLSL-----DQ 347

336 IQQQVSVSLCPDDTBLLTIVRYKDLVQKLKILRQELSQQ--OPOAGHCRLEVSREIEEE 405

348 QQQQVSVSLCPDDTBLLTIVRYKDLVQKLKILRQELSQQ--OPOAGHCRLEVSREIEEE 405

385 -----NFOQYRDFRRFLYF---ISQPAHPLPZQCHIKVRNRHIFD 425

406 SYROMKMRKPDLMXRMKLMKFRGEGEGLDGGYAREMYLISHMIMPYGHFOYSRDDY 465  
 426 SYAEMRQSATDLKRLMKFDGDDGLDGGSLREYTFCHMPPFCYLFEYSSVDNY 485

466 TLQINPDSAVNPHEIISYFHVGIMGMVAEHYIDGQFTDEPKOLIGKSLTIDDMELV 525  
 486 TLQINPHSGINPENIINYFKPFGVIGIAIFHERFDVAFVSYKMLQKVTQDMESM 545

526 DPDLHNSLWILENDITGULDHPCVHNAGBIIQBLKPGKS.PVNBNENKEYVRDY 585  
 546 DAEYTRSLWILNDITGULDHPCVHNAGBIIQBLKPGKS.PVNBNENKEYVRDY 605

586 VNWRELRGLEAQFLAQKGENVIPQHLLKTPEKELELIIGLGRIDYNDWKNTRLKH 645  
 606 TVW-IQKRIEEQOFNAFHGSFSELIPQELINVDERELLIGGSIIDMDWKGHDFRS 664

646 CTPDNIVKWWKAVEFFDEERARLLOFGTGSRYBLQGFKAQGAAGRPLFHQIDA 705  
 665 YSENQIICWFWLMDENSNEKSRLLOFTGTSRFVNGKDLQSDGPKFTIEKAGE 724

706 CTNNPLKAHTCFNRIDIPPEYESKLYEKLLTAIEETCGFAVE 748  
 725 -PNKPKAHTCFNRLDPPTSKDDDEKLSTAVEETIGFQOE 766

SUIT 5  
 Sequence 6, Application US/08895601  
 Patent No. 6060262  
 General Information:  
 Applicant: Bear-Romero, Peggy  
 Applicant: Strach, Peter J.  
 Applicant: Glass, Susan J.  
 Applicant: Rolfe, Mark  
 Title of Invention: REGULATION OF KAPPA, B (1'KB) DEGRADATION,  
 Number of Sequences: 16  
 Correspondence Address:

ADDRESSEE: FOLEY, HOAG & ELLIOT LLP  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109-2170  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/895,601  
 FILING DATE: 16-08-1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Vincent, Matthew P.  
 REGISTRATION NUMBER: 36,709  
 REFERENCE/DOCKET NUMBER: MIV-096.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-832-1000  
 TELEFAX: 617-832-7000  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 927 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 US-08-895-601-6

Query Match 33.5%; Score 1354.5; DB 3; Length 927;  
 Best Local Similarity 34.0%; Pred. No. 5.1e-118; Mismatches 232; Indels 285; Gaps 28;  
 Matches 329; Conservative 123; N mismatches 232; Indels 285;

4 PGRRRGPV-----  
 13 PGRGRARPVCVKRSEMATACTAVEVGLLEDIBENSIVRVVIAGLARKDILGASDPVYR 72

39 VV---VDGSSQCHSSTDYTKNTLDPKW-----QH-----YDLYIGK 71  
 73 VTYLDPMNGVLTSTQTKTJKSLNPKNNEBILFRVHPQGHRLIFEVDENRLTRDDPFGQ 132

72 SD---SVTISWN-----HKKIHLRKCGAGFGCYRLLSNAINRLKDTGYQRL 115  
 133 VDVPVPLPTENPLRERPYTFKDVDTHPRSHSKRSVKGYI-----RUKMT-----176

116 DLCKLGENDNDTIVRGIVVLSQSSDRIGTGGQVWD-----C---SRLFDNDLPGWBERR 167  
 177 YLPKTSGSED-----NAQOEELLEFGWVVLDDOPDAACHLQQQEPSPUPGWBWERQ 228

168 TSGRIQYLNHHTRTOWERPT-----RPASE-----194

229 DILGRYYVHNESTQWRKRTPDNLTDAGENIOLQAQRAFTTRQISEETEVSYDNQE 288

195 ---YSS---PGRPLSCFVDENTPIGT-----NGATCGQSSDPR 227  
 289 SSEANWBIREDATMYSQAFPSPPSSNLDVPTHLABELNARLTIFGNSAVSQASSN 348

QY 228 LAERR-----VRSQRHNM-----SRLHHTPD- 252  
 Db 349 HSRRGSLQAYTFFEQPTLPLPTSSGLPPGMWEIRNTATGRVYFDENRNR 408

QY 253 ---LPEGYBORTTQGQYFLH 271

Db 409 QATVETSQTSQSSAGPQSOASSTSDSGQVTOSEIROLGPLPKGNEWVHPNGRFFPD 468

QY 272 TGTGVSTWHDR--VPR-----DLSNINCBLGPPLPGWEIRNTATGRVYFDENRNR 321

Db 469 HNTKTTWEDPLKITPAHLRGKTSOLDTN---DLGPPLPGWEIRNTDGRIFYINNIK 524

QY 322 TTQFDPRLUSANLYLVNLQNOLKDQQQCVVLLCPDDECTUVP--YKRDIVQKUIL 379

Db 525 RTQWEDPL-----ENVAITGPAVPSRDYKRYEFF 556

380 RQELSQOOPQAGHCRIEVSREBIEFESYQVMKRPKDLMK-RLMIKERGEGGLDYGVA 438  
 557 RRDLKCONDIPNKFMLRRAVLESDYRTEIMGVRADPFLKARWTFGEKSLDYGVA 616  
 439 REWLILSHEMINPNTYGLFOYSRDIYTQLQINPAV-NPEHLSYFHFGGRINGMAYERPG 497  
 617 REWFPLTSKEMENPNTYGLFEYSATDNTQINPNGLCNEHDLSYFKFGRYMAYTHG 676  
 498 HYDGGTLPFLPKLQKLGSTTDDMLVDDPLHNLWLIENDITGLDHTFCYEHNAYG 557  
 677 KLDGFTRPFYKMLHKPITLHDESEVSEYNSLRWLIENDPT-ELDLRFIDBELFG 735  
 558 ELIQUHLRKGKSIPIYNEENKEYYRLVYNNWRFLRGIEAQFLAQGFNEVIPQHLLKTF 617  
 736 QTHQHELKNGSETTWNTNKKEYYLVIVQNRFYTRIQCOMAAKEGJFELLFDLXKIF 795  
 618 DEKELLELICIGLKDUDNDKVNTRLKH-CTPDNSIVKWNKAVEFFDEERRARLQFVT 676  
 796 DENELELLMCGLGDVDNDWEHTKRYKNGYSAHHVQFWKAVLMMDSERKTRLQFVT 855  
 677 GSSRVPLOGFTALOGAAGPRIFTIHQIDACTNNFKANTCERNIDIPYYESEKLYEKLL 736  
 856 GSSRVPNGPFAFLYGSNGPQSFTVOW-GTPEKLFRATHCFNRDLPPYESPEELWDKLQ 914  
 737 TAIEETOGF 745  
 915 MATEINTQGF 923

SU LT 6  
 -08-53-9-205A-6  
 Sequence 6, Application US/08539205A  
 GENERAL INFORMATION:  
 APPLICANT: Beach, David H.  
 APPLICANT: Caliguri, Maureen  
 APPLICANT: Neisky, Bradley  
 TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY, HONG & ELIOT LLP  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109-4170

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/539,205A  
 FILING DATE: 04-OCT-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Vincent, Matthew P.  
 REGISTRATION NUMBER: 36,705  
 REFERENCE/DOCKET NUMBER: CSV-005.01  
 TELEPHONE: (617) 832-1000  
 TELEFAX: (617) 832-7000  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 834 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Query Match 33 5%; Score 1333; DB 3; Length 834;  
 Best Local Similarity 44.6%; Pred No. 6e-118;  
 Matches 275; Conservative 93; Mismatches 188; Indels 60; Gaps 12;

Qy 159 LPDGWEERRTASSGRIGQYLNHITATTOWERPTPASEYSSPG----RPLS 203  
 Db 246 LPSCHWEERDKAKGRTTYTNHNNRTTTRPINQLAEDGASATSNHLLEPQIRRPRS 305  
 Qy 204 C---FVDENTPISSNTGATCQGSSDPRIAERVRVSQHRNTMSRTHLHTPDLPEGYEAR 260  
 Db 306 LSPSPVTLTSALEAKADSPPVRAVKDTLNSPQPSPYNSPKPQHKVTKQSFLPPWENR 365  
 Qy 261 TTOCGQVFLHTQGVSTMHDPPVP----RDLSNINCEELGPLPPGMWIEIRNTATGRVYF 315  
 Db 366 IAPNGRPFIDHNTKTIWEDPLKFPHMRSKTSLSNENDLGPLPPGWEERIHLDGRTFY 425  
 Qy 316 VDHNNRTQFTDPLRSANLHLVLRNQNOLKOOQQQVVSCLCPDDTCBLTVPR-YKRDLV 373  
 Db 426 IDHNSKITOWEDPL-----QN-----PAITGPAPVPSREFK 457  
 Qy 374 QKLKLRQBLSQOPOQACHCRILEVSREEIFERSYQWMKRPKDLMK-RLMIKFPGEEGL 432  
 Db 458 QKDYFRKLKKPZADIPNRFEMKLHRNNTPESYRRLMSVTRPVKLRWLIEFEKGL 517  
 Qy 492 MAVPHGYIDGGFTLPFLPKLQGKSTTDDMLVDDPLHNLWLIENDITGLDHTFCV 551  
 Db 578 LAVPHGKLIDGFFTRPFYKMLGKQITLNDMESEYNSLKWILENDT-ELDLMFCL 636  
 Qy 552 EHNAEGTIOQHELKPGKSGTIPYNEENKEYYRLVYNNWRFLRGIAQFLAQKGFNEVIPQ 611  
 Db 637 DEENFGQTYQVDLJKPGESEIMTENREYIDLVIQWRVQKOMNAFLEGFTELLPI 696  
 Qy 612 HLTAKTDFEKELEIJIIGGKGDYDNMKVNTLK--HCTPDSNIKWNKVAEEFDEERA 669  
 Db 697 DLXIKFDNNELELMCGGDVNDNRQHSITYKGYC-PNHPVNFMKAVLNDAEKII 755  
 Qy 670 RLOFVGTGSSRVVLOGFKALQAGPRLFTHQIDACTNLLPKAHTCFNRDIPYSES E 729  
 Db 756 RLQFVGTGSSRVVLOGFKALQAGPRLFTHQIDACTNLLPKAHTCFNRDIPYSES E 814  
 Qy 730 KLYEKLILAISETCGF 745  
 Db 815 DLREKLIMAVENAQGF 830

RESULT 7  
 US-09-392-163A-6  
 ; Sequence 6, Application US/09392163A  
 ; Patent No. 6503742  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beach, David H.  
 ; APPLICANT: Caliguri, Maureen  
 ; APPLICANT: Neisky, Bradley  
 ; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FOLEY, HONG & ELIOT LLP  
 ; STREET: One Post Office Square  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109-2170  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; SOFTWARE: PC-DOS/MS-DOS  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/539,205A  
 ; FILING DATE: 04-OCT-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Vincent, Matthew P.  
 ; REGISTRATION NUMBER: 36,705  
 ; REFERENCE/DOCKET NUMBER: CSV-005.01  
 ; TELEPHONE: (617) 832-1000  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 834 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/392,163A  
 ; FILING DATE:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/539,205

FILING DATE: TITLE OF INVENTION: Ligase  
 ATTORNEY/AGENT INFORMATION: NUMBER OF SEQUENCES: 11  
 NAME: Vincent, Matthew P. CORRESPONDENCE ADDRESS: ZENECA Pharmaceuticals, Inc.  
 REGISTRATION NUMBER: 36,709  
 REFERENCE/DOCKET NUMBER: CSV-005.01  
 STREET: 1800 Concord Pike  
 TELECOMMUNICATION INFORMATION: CITY: Wilmington  
 TELEPHONE: (617) 332-1000 STATE: DE  
 TELEX/FAX: (617) 832-7000 COUNTRY: USA  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 834 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein -09-392-163A-6

Query Match 33 5%; Score 1353; DB 4; Length 834;  
 Best Local Similarity 44 6%; Pred. No. 6e-118;  
 Matches 275; Conservative 93; Mismatches 188; Indels 60; Gaps 12;

159 LPDGEBERRTASGRQYLAHITRTRTQEWBPTRASEYSSP-----RPLS 203  
 246 LPSGNNEERKDAKGRTYYVHNRRITWTRPIMLAEDGASGATNSNNHLIEQIRPRRS 305  
 204 C---FVDTPIISGNTAGCGSSDPRILERRRSQRHRNYSRSRTHTPPDLPBGEYQR 260  
 306 LSSPTVTLSAPLEGAKDSPTYRAVTDLSNPQSQQSPSYNSPKQHKYTQSFLPPWNER 365  
 261 TTQGQGYFYIHTOTGSVSTWHDPRYP----RDLNSINCBEGLPQGMWEIRNTATGRYVF 315  
 366 IAPNGRPFFIDHNTKTTTWDPRLUKPPVEMRSKTSIISANNDLPLPPWEERTHLDGRTFY 425  
 316 VDHNNRTTOFTDPRLSANLHLVLRNQNQLKDQOCQQVYSLCDDTECLTVPR-YKRDVL 373  
 426 IDHNSCTIQEDPRI-----QN-----PAITGPAPVPSREFK 457  
 374 QKLKLIQELSQQQDQAGCHRISREEIFEEYSRQMKMQRPKDLWK-RLMKFKPSEGK 432  
 458 QKDYFRKLUKKPAIDPNRFEMKLHRRNIFEEYSRTRMSVKREDVLKARLWEPFEEBKGL 517  
 433 DYGGAAREWLYLSEBMNAPYGFQYSSDITLQINPDSAV-NPBLPSYHFVORIMG 491  
 518 DYGGTAEWFLLSEMEMPYGYGFQYSSDITLQINPNSGICNCEHLSFTFIGRVAG 577  
 492 MAVFHCHYDGGTFPLPKOLGKSITLDMELVDPDHLNSLYLWILENDITCVLDTFCV 551  
 578 LAVFGCKLJLUFFFPFYKMLGQQTINNDMESTDEYINSLKWLLENDPT-ELDLMFCI 636  
 552 EHNAYGEIIQHELKNGKSIIVDENKEKEYVRLLYVNTWRFLRGTEAQFLALQKGNEVIPO 611  
 637 DEENFGTYQVDLKGNSEIMVNENKEVYDLYQWRFVNRVQRQNNAFLEGFTLPI 696  
 612 HLLKTFDEKLELICLGKIDYNDWKNTRLK-HCTPDSNIYKNEWKAIEFDEBERRA 669  
 697 DLKJFDNEJELINCGLGDVYDNDWQHSIYNGYC-PNHENVQFWKAITLMDAEKRI 755  
 670 RLQFYTGSSRVPLQGKALOGAGPRLFTIHQIDACTNNULPKAHTCENRDIIPYESYE 729  
 756 RLLQFYTGSSRVPLQGKALOGAGPRLFTIHQIDACTNNULPKAHTCENRDIIPYESYE 814  
 730 KLYEKULITAETTCF 745  
 815 DLREKLMAYENAQQF 830

Query Match 33.1%; Score 1336; DB 2; Length 854;  
 Best Local Similarity 36.6%; Pred. No. 2.5e-116;  
 Matches 316; Conservative 130; Mismatches 272; Indels 146; Gaps 24;

13 KLRITVLCAK-NLVKDKDFRPLPDKFAKUVVYDGSQCHSTDVTXMTLDPKWNQHYDLYIGK 71  
 9 QLQITVSAKLUKENKCNWFG-PSVPEVTD--GQSJKTEKCNNTNSPKWKOPITVVTP 65  
 Db 72 SDVTISWNHKKHHK-K-QQAGFLGCVRLLSNAIRNLKDTGVRDLCKLGPNDNDTVR 129  
 Db 66 TSKLCPFVWSHOTLKSDSLVLGTLGDIYETLKSNMCKLEEV--VMTLQLVGKBEPEPTM 122  
 Qy 130 GQTVV--SLOQSRDRIGTGGGV-----DCSRLDNDLDP-----GWBE 165  
 Db 123 GDSVCLDGLQVEAVVNGETCSSESTONDDGCRTRDTRIVSTNGSEDPEVAGENK 182  
 Qy 166 RRTASGRQIYLNHHTRTOWERPRTPAEYSSSPRPLSCFVIDENT-----PIS 213  
 Db 183 RANGNNPSLSNGGFKRSRPRSRPPP--PTPRPASVNGSPTNSDGSSTGSLPPT 240  
 Qy 214 GTIN-----GATCG-----QSSSPRLAERRRSQRHNM-----242  
 Db 241 NTVNTNTSETSEGATSGIIIPUTISGSSGPRLNTSQAPIUPGWWQRV-DQHGRVYYDV 299  
 Qy 243 -SRTHLHTPPDLPPEGYQRTTQGQVYFLHTQTGSTWHDRPV-----285  
 Db 300 EKRTTWDRPEPLPGMTERYDNMGRIYYTDHFTRTTMRPTLESVRATEQWQLQRSQI 359  
 Qy 286 -----RDL-----SNTCEELGPLPQGMWEIRNTATGRYVFYDHNRTTQPTD 327  
 Db 360 GAMQFNQRFLYGNQDLFATSONKEFDPLGPLPQGMWERTDNSNGRIVYVNHNTITQWED 419  
 Qy 328 PRISANLHLVNRNQNLKDQCCQVVSLLCP---DDTBCLTV--PR-----Y 368  
 Db 420 PRSQGQ---LNEKPDPGWEMLRFTVTDGIPYFVDBHRNRRATTYIDPRIGKSALDNGPQIAY 475

SULT 8  
 -09-070-060-4  
 Sequence 4, Application US/09070060  
 Patent No. 5976849  
 GENERAL INFORMATION:  
 APPLICANT: Hustad, Carolyn M.  
 APPLICANT: Ghilday, Namit  
 TITLE OF INVENTION: Human E3 Ubiquitin Protein

369 KRDLVQKULKILR---QELQQPOAQGHCRIEVSREEIFEESEYRQWQKMRPKDJWKRIMIK 425  
 476 VDFFAKVQFREFWQQLAMPQ---HKITVTRKTFEDSFQINFSFSPDLRERLWVI 531

426 ERGEGLDYGGVARBWLILSHMLNPYGLPQYSRDIYLTQINPDSANAPHELYPHF 485  
 532 FPGBEGLDYGVARWFULLSHEVNLNPYCLFYAGKDNYCLOINPASYLNDHLKYPFRF 591

486 VGRIMGMAYFHGYTDGGFTLPFYKQLQGKSTLDDMELVDLASHSLWTLENDTGTV- 544  
 592 IGRFFAMALPHGKFDTGSLSLPYKRILNKPSLKDSEPEYNLSLWTKENNLEECG 651

545 LDHTPCVEHNAYGBTQHBLKPNSRSPVNEENKEVRLYNNWRFLRGIBAQFLALQKG 604  
 652 LEMTIVSDKEILGEKSILKPKNGNLYTEENKEVIRMYAEWRSRGVEBTQAFPEG 711

605 FNEVLPQHLLRTFDEKELELLIICGLGKIDNDWKVNTRLKHTPDSONIVKRMKAVEFFD 664  
 712 FNEIPDQQLQYDFDAKELEVLLCMQEIDLNDQRHALYRHYTRTSKQIMMFWQFREID 771

665 EERRARLQLQTYGSRVPLQGXKALQGAAGPRIFTHQIDACTNNUPKAHTCNCENIDIPP 724  
 772 NEKRRLLQEVGTGTRLPYGFADLMGSNGSPQKFCITERVK-ENWLPRSHTCFCNFLDPP 830

725 YESPYKLYEKULTAETETCGFRAVE 748  
 831 YKSYSQLKEXLILFALEETEGFGQE 854

SULT 9  
 -09-357-746-4  
 Sequence 4, Application US/09357746  
 Patent No. 608122  
 GENERAL INFORMATION:  
 APPLICANT: ZENECA Limited  
 TITLE OF INVENTION: HUMAN E3 UBIQUITIN PROTEIN LIGASE  
 FILE REFERENCE: PHM 70312\_N1  
 CURRENT FILING DATE: 1999-07-21  
 EARLIER APPLICATION NUMBER: US No. 6087122 60/073, 839  
 EARLIER FILING DATE: 1998-02-05  
 EARLIER APPLICATION NUMBER: US No. 608712209/070, 060  
 SOFTWARE: FastSeq For Windows Version 3.0  
 SEQ ID NO 4  
 LENGTH: 854  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 -09-357-746-4

Query Match 33.1%; Score: 1336; DB: 3; Length: 854;  
 Best Local Similarity 36.6%; Pred: No. 2.5e-116;  
 Matches 316; Conservative 130; Mismatches 272; Indels 146; Gaps 24;

13 KLRITVLCAK-NLVKDFFLPDPFARYVVDGQCHSTDYVNTLDPKRNQHYDLYIK 71  
 9 QLQITIVISALKKENKKNWGS-PSTPVETVD--GQSCKTEKNNNTSPKWKQPLTVTVP 65  
 72 SDSVTISVNHKKTHKK--QGAGFLGCVRLLSAINFLKDGYQRLDLCKLGNDNDTyr 129  
 66 TSKLCFWRVSHQTLKSDVLLTAGDIYETLSNNMKLEEV--VNTLQLVGDKSEPETEIM 122

130 GQIVV--SIQSRDRDITGTCQVV----DCSPLFEDNDLPD----GWEE 165  
 123 GDLSVCLDGQVAEVTINGETSSSSTQNDDGCRTRDDTVSTNGSEDPEVAASGENK 182

166 RRTASORIOLNHHTTRTOWERPRTPASEYSSPGRPLSCFVDENT-----PIS 213  
 183 RANGINSPSIUNGKTPSPRPRPPP--PTPERRPSVNGSPSTNSDSDSSTGSLLPT 240

214 GTN-----GATCG-----QSSDPRLAERRVRSQRHRNTM-----242

Db 241 NTVNTSTSEGATSGLIPLTISGSGPRPLNTSQAPLPPGWQVR-DQHGRVYVDHV 299  
 QY 243 -SFTHLHTEPDLPGEQRTTOQGOVYFLHTQGYSTMHDPRVP-----285  
 Db 300 ERTTWDRPEPLPGERRDVNMGIYVHDHFTRTTWORTPLSSVRYTEQWOLQRSOLQ 359  
 QY 286 -----RDL-----SNINCBEGLPLPCEWEIRNTATORGRVYFDENNRRTQFTD 327  
 Db 360 GAMQFNQRFTYGNQDLFATSQNKEFDPLGPLPPOWERKFTDSNRVYFVNHTRTRQED 419  
 QY 328 PRISANLHLVILNQNOLKDQQQQVQVSLCP--DDTECTV--PR-----Y 368  
 Db 420 PROQO---LINEKPLPEGMFRFTDGLAPYFVUNHRRTATYDPRTGKSALDNGPQIAY 475  
 QY 369 KRDLVQKLKLR---QELSOOPQDAGHCRLVESSBEEFESYRQVMKRPDKDWMKRMK 425  
 Db 476 VRDFKARVOYPRFWCQQLAMFO---HIKTVTRKTLFEDSFQOIMSFSQDLRBLWVI 531  
 QY 426 FREGEGDYGGAERYLILSHEMINPYGLFQYSRSDDTYLOINPDSAVNPHELSYHFP 485  
 Db 532 PPEEGDYGGAERYFFLISHEVNPMCLFEAGKONVYCLQNPASYINPDLYKYRFP 591  
 QY 486 VGRIMGMAVFHGYTDGGFTLPFYKOLLGKSTSIDDMELVDPDHLNSLWILENDITGV-  
 Db 592 IGFIAWALFKFKIDTGFSLPFYKRLNKPVGKDLBSIDPETYNSLIVKENNIEBCG 651  
 QY 545 LDHTFCYHNAYGEIYQHEKPNQGSIPIVNEENKEYVLYNNWRFLGIEAQFLALQKG 604  
 Db 652 LENYFSYDKEIYGETKSHDJKPGNQNLTYEENKEYTRVNAEFLRSGEVECQQAFFEG 711  
 QY 605 FNEVIPQHLLKTDEKELELLIICGLGKIDNDWVNTRLKHCPDSNIVKMFNKAVEFPD 664  
 Db 712 FNEILPQOQYLFDAKELEVLLCMQEIDLNDQRHALYRHYTRTSKQIMMFWQFREID 771  
 QY 665 EERPARLQLQFTGSSRVPLOGPKALOGAQAPRLFTHQIDACTNLPKHTCPNRIDIPP 724  
 Db 772 NEKRMRLQFTGTCPLPVGSFADLMGSNGSPQKFCITERVK-ENWLPRSHTCTNRLDIPP 830  
 QY 725 YEYERKLYEKULTAETETCGFATE 748  
 Db 831 YKSYEQULKELKLFABETEGFGQE 854

RESULT 10  
 US-09-070-060-3  
 ; Sequence 3, Application US/09070060  
 ; Patent No. 5976849  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Russad, Carolyn M.  
 ; ADDRESS: Ghildyal, Nanit  
 ; TITLE OF INVENTION: Human E3 Ubiquitin Protein  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; STREET: 1800 Concord Pike  
 ; CITY: Wilmington  
 ; STATE: DE  
 ; ZIP: 19800-54337  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/070, 060  
 ; FILING DATE: 30-APR-1998  
 ; CLASSIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/073, 839  
 ; FILING DATE: 05-FEB-1998

ATTORNEY/AGENT INFORMATION:  
 NAME: Higgins, Patrick H  
 REGISTRATION NUMBER: 39,709  
 REFERENCE/DOCKET NUMBER: PHM-70312  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 302.886.4889  
 TELEFAX: 302.886.8221  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 852 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: Unknown  
 MOLECULE TYPE: Peptide  
 -09-070-060-3

Query Match 32.9%; Score 1329; DB 2; Length 852;  
 Best Local Similarity 33.8%; Pred. No. 1. 1e-15;  
 Matches 306; Conservative 129; Mismatches 240; Indels 230; Gaps 20;

13 KLRATVLCR-NLVKDFRLPPEAKWVVDQGCHSTDTVKNTLDPKWNQHDLYIK 71  
 9 QLQIVAVISALKENKENKNGE-PSPYEVTVD-GQSKRKTERCNNTNSPKRKQPLTVIVTP 65  
 72 SDSVTISWKKKTHKQGAGFGCVRL-----99  
 66 VSKCHFRWSHOTL--KSDVLLGTAALDIYTLLKNNMKLEVVVTLQGGDKEPTEI 122  
 100 -ISNAINRLK-----DTGYQLDLCKLGNDND-----126  
 123 GDLSCLDQIOLSEEVVNTGETTCSESASQNDGSRSKDETRVSTGSDPDAGENR 162  
 127 -----TVRGQIVVLS-----138  
 183 RVSGETNSPSLSNNGGFKPSRPRPSRPPRPSRPPPTPRPASTGSPSATSSESDGSSTGSLPPPTN 242  
 139 -----RDRIGTCQV-----VDCSRL 154  
 243 NTNTSEGATSGLLIPLITSGGSDPRPILNPUTQAPIIDPGWERVDDGRVYVDRFTERRT 302  
 155 FD--NDLPDGWEERTASGRIOTLNHTTRTOWERPT---RPASEYSSPGRPLSCFYDE 208  
 303 WDRPDPPLPGWERVDDNGRIVYVDDHTRTTWQRPIPLESYRNVEWQLORSQI-----356  
 209 NTPISGTNGBACGOSSDPRLAERVRSSORHRYNMSRTHLHTP-PDLEGXEQRTQQV 267  
 357 -----GAMCQFNQFIFYGNQDLPATSSKEFDPLGPPIPGEKRTDSNGRV 403  
 268 YFLHQTGYSTWDPRVERDLSMINCEBLGPPGEGIRNTATGRVYFUDHNNRTTQFD 327  
 404 YFVNHRINTRTOWERPSSQOLNE----KPIPEGEMRFYDGFYFVDHNRRTYID 457  
 328 PRLSANLHLVNRONQLKDQQQQVVSCLPDDTECLTVPRYKDLVKQKILR--QEDS 384  
 458 PRTGKS--ALDNGPQI-----AYVRDFKAKYQYPRFMQQLA 492  
 385 QQPDAHGCRIEVSREEFEESYRQUNMRKPDLNKRLMIKPRGEEGLDGGVAREWYL 444  
 493 MPQ-----HKITVTRKTLFEDSPQOINSFSPODLRKLWTFPGEGELDGGVAREWFFL 548  
 445 LSHMLNPYYGLFOYSRDUITYLQINPDSAVNPEHLSYFHVGRTMGMAVFGHYTDGSF 504  
 549 LSHEVLNPMPCLFPEAKDNYCLQINPASYINPDHAKYFRIGRFJAMALFRKFDTDF 608  
 505 TLPPFKQJLGKSTLDDNELLVDPDLHNSLWILENDITGV-LDHTFCVHENAYGBIIOHR 563  
 609 SLPPFKRNLNPCLFPEAKDNYCLQINPASYINPDHAKYFRIGRFJAMALFRKFDTDF 668  
 564 LPNGKSPISPYNEENKEYTRLYNMRFLRGIAQFLQKFNEYIPQHLLKTSDEKELE 623  
 669 LPNGKSPISPYNEENKEYTRLYNMRFLRGIAQFLQKFNEYIPQHLLKTSDEKELE 728

Qy 624 LTIICGLGKIDYNDWKVNTRLKHCTPDSNIVKWFKAEEFDEERARLQFYTGSSRVPL 683  
 Db 729 VILCGHOEIIDNDWQHAIYRHYARTSKCIMWFQVEIDNKRMRILLQFTGTCRLPV 788  
 Qy 684 QGFKAQOGAAQPRPLPITHQDACTNLPKAHTCNRDIPPSYEKLYEKULATAETC 743  
 Db 789 GSFDLINGSNGPQKCFTEKVKG-ENWLPRSHTCNRDLPYKSYEQLKULFAEBETE 847  
 Qy 744 GFANE 748  
 Db 848 GFQQE 852  
 RESULT 11  
 US-09-157-746-3  
 ; Sequence 3, Application US/09357746  
 ; Patent No. 6087122  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ZENECA Limited  
 ; TITLE OF INVENTION: HUMAN E3 UBIQUITIN PROTEIN LIGASE  
 ; FILE REFERENCE: PBM-70312, N1  
 ; CURRENT APPLICATION NUMBER: US/09/557,746  
 ; EARLIER APPLICATION NUMBER: US No. 6087122 60/073,839  
 ; EARLIER FILING DATE: 1998-02-05  
 ; EARLIER APPLICATION NUMBER: US No. 608712209/070,060  
 ; EARLIER FILING DATE: 1998-04-30  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 852  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-157-746-3  
 Query Match 32.9%; Score 1329; DB 3; Length 852;  
 Best Local Similarity 33.8%; Pred. No. 1. 1e-113;  
 Matches 306; Conservative 129; Mismatches 240; Indels 230; Gaps 20;  
 Qy 13 KLRATVLCR-NLVKDFRLPPEAKWVVDQGCHSTDTVKNTLDPKWNQHDLYIK 71  
 9 QLQIVAVISALKENKENKNGE-PSPYEVTVD-GQSKRKTERCNNTNSPKRKQPLTVIVTP 65  
 72 SDSVTISWKKKTHKQGAGFGCVR-----99  
 66 VSKCHFRWSHOTL--KSDVLLGTAALDIYTLLKNNMKLEVVVTLQGGDKEPTEI 122  
 100 -ISNAINRLK-----DTGYQLDLCKLGNDND-----126  
 123 GDLSCLDQIOLSEEVVNTGETTCSESASQNDGSRSKDETRVSTGSDPDAGENR 162  
 127 -----TVRGQIVVLS-----138  
 183 RVSGETNSPSLSNNGGFKPSRPRPSRPPRPSRPPPTPRPASTGSPSATSSESDGSSTGSLPPPTN 242  
 139 -----RDRIGTCQV-----VDCSRL 154  
 243 NTNTSEGATSGLLIPLITSGGSDPRPILNPUTQAPIIDPGWERVDDGRVYVDRFTERRT 302  
 155 FD--NDLPDGWEERTASGRIOTLNHTTRTOWERPT---RPASEYSSPGRPLSCFYDE 208  
 303 WDRPDPPLPGWERVDDNGRIVYVDDHTRTTWQRPIPLESYRNVEWQLORSQI-----356  
 209 NTPISGTNGBACGOSSDPRLAERVRSSORHRYNMSRTHLHTP-PDLEGXEQRTQQV 267  
 357 -----GAMCQFNQFIFYGNQDLPATSSKEFDPLGPPIPGEKRTDSNGRV 403  
 268 YFLHQTGYSTWDPRVERDLSMINCEBLGPPGEGIRNTATGRVYFUDHNNRTTQFD 327  
 404 YFVNHRINTRTOWERPSSQOLNE----KPIPEGEMRFYDGFYFVDHNRRTYID 457  
 328 PRLSANLHLVNRONQLKDQQQQVVSCLPDDTECLTVPRYKDLVKQKILR--QEDS 384  
 458 PRTGKS--ALDNGPQI-----AYVRDFKAKYQYPRFMQQLA 492  
 385 QQPDAHGCRIEVSREEFEESYRQUNMRKPDLNKRLMIKPRGEEGLDGGVAREWYL 444  
 Db 505 TLPPFKQJLGKSTLDDNELLVDPDLHNSLWILENDITGV-LDHTFCVHENAYGBIIOHR 563  
 Qy 567 -----QGAMQFNQFIFYGNQDLPATSSKEFDPLGPPIPGEKRTDSNGRV 403  
 575 FD--NDLPDGWEERTASGRIOTLNHTTRTOWERPT---RPASEYSSPGRPLSCFYDE 208  
 303 WDRPDPPLPGWERVDDNGRIVYVDDHTRTTWQRPIPLESYRNVEWQLORSQI-----356  
 209 NTPISGTNGBACGOSSDPRLAERVRSSORHRYNMSRTHLHTP-PDLEGXEQRTQQV 267  
 357 -----QGAMQFNQFIFYGNQDLPATSSKEFDPLGPPIPGEKRTDSNGRV 403  
 268 YFLHQTGYSTWDPRVERDLSMINCEBLGPPGEGIRNTATGRVYFUDHNNRTTQFD 327  
 404 YFVNHRINTRTOWERPSSQOLNE----KPIPEGEMRFYDGFYFVDHNRRTYID 457  
 328 PRLSANLHLVNRONQLKDQQQQVVSCLPDDTECLTVPRYKDLVKQKILR--QEDS 384

458 PRTGKS --ALDNGPQI-----AYRDFAKVQYFRWCCQLA 492  
 385 QQPQAOCHCRLVESSREBIEFESYRQVMKRPDKLURMINKFGEGLDYGGVARYNLYL 444  
 493 NEQ---HIKTIVTRKLFLFEDSFQOIMSFSPQDLRRLWVIFGEGLDYGGVARYNRFEL 548  
 445 LSHEMANPYGYLGFQSRDDYTILQNPDSAVNPBLSPHVFGRGMGVAFGHYIDGPF 504  
 549 LSHEVANEMCYLFEEAGKDNCLQNPASVNPBLKTYPRFGTETIAALFKPDTGF 608  
 505 TLPPFYKOLLGSKITLDDMELYDPDILENSLVWLENDITCV-LDHTFCYEHNAYGEIQTQE 563  
 609 SLPPYKRILKPVGKLDLSDEPEYNSLIWKENNIECEDLMYFSYDKEIIGEKXSHD 668  
 564 LKPNGSISIPYNEBNKKEYVRYLVNNTRFLRGIEAQFLAOKGNEVTPQHLKTEDKEKELE 623  
 669 LKPNGGMLVTEENKEBYIRNAEFLRSVGEBOQAPEGFNBILPQYLOFDAXELE 728  
 624 LLIICGKGKIDYNDWKNTNTRKHCTPDSNIVKMFNKVAEEFDEERRARLLOPFTGSSRVPL 683  
 729 VLLCGQEBIDNDWQHATYHRARTSKQMMWFQVKEBDINKRMRLLOPFTGCRLPV 788  
 684 QGPKAQOGANGPRLPTFIHQDACTNINLPKAHTCNCRIDIPPYESYKELYEKULTABETC 743  
 789 GCFADMGNSNPQKCEKRYGK-ENWLPSHTCENRLDLPPTKSYEQLKEKULFAEETE 847  
 744 GFAVE 748  
 848 GFGQZ 852  
 SULT 12-08-630-916A-48  
 Sequence 48, Application US/08630916A  
 Patent No. 6011137  
 GENERAL INFORMATION:  
 APPLICANT: Pirozzi, Gregorio  
 APPLICANT: Fowlkes, Brian K.  
 APPLICANT: Key, Dana M.  
 TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
 TITLES OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
 NUMBER OF SEQUENCES: 1244  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1105 Avenue of the Americas  
 STATE: New York  
 COUNTRY: United States  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08-630-916A  
 FILING DATE: 03-APR-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MIRSKO, S. LESLIE  
 REGISTRATION NUMBER: 18-872  
 REFERENCE/DOCKET NUMBER: 1101-10-203  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 896-8864/9741  
 INFORMATION FOR SEQ ID NO: 48:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 906 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: Peptide  
 08-630-916A-48

Query Match Score 1298.5; DB 3; Length 906;  
 Best Local Similarity 42.0%; Prec. No. 98-113;  
 Matches 211; Conservative 101; Mismatches 216; Indels 57; Gaps 9;  
 Matches 271; Conserv. 101; Mismatches 216;  
 122 PNDNDTVRSQIVVSLSQRDRGQVQVDCSRLFDNDLPGWEERTASGRIOQLAHITR 181.  
 Qy 301 PNPNNTSLSPAPATPAEGEPSTGQOLPAAAQAPPALPAGWEQBLPGRVYVDHNTK 360  
 Db 182 TTWERLPRTPASSEYSSPGRPLSCFDVENTPISGTNTGATCGSSDPLAERSVRSQRHNR- 240  
 Qy 361 TTWERLPLPPGWKRIDPGRYIYDENT----RTTMWQRPTAEVANYEQNSQRNQ 414  
 Qy 241 -----YMSRTHLHTP-PDLPEGYEORTTQCGQVYFLHTQGVSHTWDPRV 284  
 Db 415 LQAMQHSQRFLYQFSASTHDPLPGLPQGWKR-QDNGRVYVNFNTTQWEDPRT 473  
 PRDLSNINCEELGPLPGWEIRNTATGRUYFDHNRTRQFTDPBLSANHHLVUNRNQNL 344  
 Qy 474 QMNIQE----PALPGWENKTYTSCEVRFEDVNTRTTTFKDPRGFE----- 516  
 345 KDOQQQVSVSLCPDDTECLTVPRYRDVLQKLKIIQRELSQQQQPAQHCRIEVREEIFE 404  
 Db 517 -----SGTKQGSPGAYDERSFRNKYHQFR-FLCHSNALPSHYKISVRQTLZ 562  
 405 ESTRQVMKRPDKLWKLMIKFRGEGBLGQYGVAREWLYLSHMLNPYGLFOYSRDI 464  
 Db 563 DSFQINNMKPDLLRLYIIMRGEGLDGGIAGAEWWFLSHBYLNPWYCLFLTAGKNN 622  
 Qy 623 YCLOINPASSINPDHLTYFRFIGRFIAMJYHGKFDTGETLPYKRMLINKRPLKQDLS 682  
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 Db 683 IDEPFSNIVWKENNIEEGLYELFQDNEILGRVYTHEKEGESSTRTVEKEKYM 742  
 LYTNWREURGIAQFLALQGFSNEVAPLWLYTDEKELELIGLGKDVNWKVNTRL 643  
 Db 743 LUDWRERTRGVBEQTAFLDGFNEVAPLWLYTDEKELELIGLGKDVNWKVNTRL 802  
 644 KHCTPDNSIVKMFVKAVEFDEERARLLOFTGTSRVPQLGFFKALQGAAGRIFTIHQI 703  
 Db 803 RHYTNQSKQIQWVQVYKENDNERKIRLQFVTGCRLPYGGPAELIGSNGPQXFCIDKV 862  
 Qy 704 DACTNTNPKAHTCFNIDIPPEYESKLYKLIAEETCGFATE 748  
 Db 863 GRET-WLPRSHTCPNRLDLPYKSYEQLREKLIAEETEGGGE 906  
 RESULT 13  
 US-08-630-916A-48  
 Sequence 46, Application US/08630916A  
 Patent No. 6011137  
 GENERAL INFORMATION:  
 APPLICANT: Pirozzi, Gregorio  
 APPLICANT: Kay, Brian K.  
 APPLICANT: Fowlkes, Dana M.  
 TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
 TITLES OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
 NUMBER OF SEQUENCES: 1244  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1105 Avenue of the Americas  
 STATE: New York  
 COUNTRY: United States  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08-630-916A  
 FILING DATE: 03-APR-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MIRSKO, S. LESLIE  
 REGISTRATION NUMBER: 18-872  
 REFERENCE/DOCKET NUMBER: 1101-10-203  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 896-8864/9741  
 INFORMATION FOR SEQ ID NO: 48:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 906 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: Peptide  
 08-630-916A-48

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/630,916A  
 FILING DATE: 03-APR-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MISROCK, S LESLIE  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 1101-1-203  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 890-9090  
 TELEFAX: (212) 896-8864/741  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 683 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 -08-630-916A-46

Query Match 28.1%; Score: 1134.5; DB: 3; Length: 683;  
 Best Local Similarity 43.7%; Pred. No. 1-4e-97; Mismatches 84; Indels 45; Gaps 11;

Matches 241; Conservative 84; Mismatches 182; Indels 8 45; Gaps 11;

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159 LPDGWEERRTASGRQYLHHTTRTQWER--PTRPASEFSSPGRPLSCFVDENTPSGTN 216  
 162 LPSGEQEQRDQPHGRTYYVQDNHTRTTRWPQPPLPGWNRVDRVVYDHNTRTTWQ 221

217 GATC----GQSSPRLAERRVRSQRHRNTM-SRTHLHTPPD---LPEGYEQRTQQG 265  
 222 RPTMSEVRNEEQWQSQRNQLGAMQMQNQRQLYSASMAAENDPYGPPLPPWEKVDSTD 281

266 QVYFLHTQGVSTTHDPYPRDLSNINEEGLPQPMWEIRNTATGRVFTDHNNRTQF 325  
 282 RYFYNHNTXKTQEDPRT-QGQN--EE--PLPESWEIYTRSVRYFVDHNTRTTF 335

326 TDPRISANLHLVLNARQNQLKDDQQQQVQVVSICPDDTECLTVPPYKRDLVQKLURQELSQ 385  
 336 KDPER----NGKSSVTKGQPIA-----YERFRWKLAHPY-LCQ 370

386 QQPQGHCRLEVSBEIFEDSYRQYKMRPKDILWKRUMIKPFRGEGBEDYGGAVAREWLYLL 445  
 371 SNALPSHVKNVNSQTLFEDSFQIMALKPDYLRRLVYVFRGEGBEDYGGAVAREWLYLL 430

446 SHEMINPYGYGLFOYSRDDIYTLOINPDSAVPEHLSYFHFYGRIMMAVPHGYIDGGFT 505  
 431 SHEVINPMPYCLFEAGKNNYCLQNPASTINPHLSYFCFGRFIMALPHGFIDTGRS 490

506 LPPFKYQKLGKSKITLDDMELVDPDILHNSLWILENDITGV-LDHTPCVEMHAYGELIQLHEL 564  
 491 LPFYKMLSKSLTIRLDSEIDTEYNSLWIRDNNIBECGLEMYYFSDMELGKVTSHDL 550

565 KPNQGSIIPYNEENKEKEYYVLYVNWRPLGIEAOFLAQKGNEVILQHJLXTFDKKELEL 624  
 551 KLGNGNLTUEENKEDEYIGLMTPKFRSGVOEQTAKAFLDGFNEWVVLQLOYFDEKELEV 610

625 IICGEGKIDVNDKVNTRLKHCTPDNSIVKWWKAVERDEBRAILQFTGSRVPLQ 684  
 611 MLCGNQEVDAWQRLADWQRLNTVYRHTRNSKQIIWFWQFVKETDNEVRAKLLQFTGICRLPLG 670

685 GFKAQGAAGPR 696  
 671 GFAELMGNSGPR 682

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Query Match 28.1%; Score: 1134.5; DB: 2; Length: 874;  
 Best Local Similarity 25.1%; Pred. No. 4.9e-41; Mismatches 275; Indels 161; Gaps 23;

Matches 185; Conservative 117; Mismatches 275; Indels 161; Gaps 23;

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Qy 105 NRELKDTCYQRDLCKLQGPN---DNDTIVRGQIVVLSJQSQRDRIGT-----GQVVDCS 152  
 Db 202 SRIGDSSQGDNNLNLQKGPDIIVSVIDVIAAT-RVYVRLNNEKITAFINALVYLSPTVCD 260  
 Qy 153 RLFDNDLPLDGMWBERRTASGRIQYLHHTTRTQWERPRTPASEFSSPGRPLSCFVDENTPI 212  
 Db 261 IYHN-----VYSRDPNVLNF--IIGMENRNLHSPEYTEMALPLPKAMSKLPL 308

Qy 213 SGTN-----ATCGQSSDPLRAERRVRSQRHRNTMYSRTHL-----247  
 Db 309 AAQGKJIRLWSKYNAQDQIRRMETFQQLITYKVINSNEFNSRNLYNDDAIV 368

Qy 248 -----HTPPD---LPE-----GYEORTTOQGQYFLH 271  
 Db 369 ASRKCLKMYVANUQGEVDTNHEDDEPIASSELTLQELGEBRNKQGLRVDPFL 428

Qy 272 TGTGSTWHDPVPDLSNINCEELGPLPGWERTNTATGRV-----YFVDHNNT 322  
 Db 429 TELGVK-----LDCRK-----PLPSEETINEPANEVLEMDDYTFKVBETBNKF 474

Qy 323 TQFTDPRI--SANLHVLNQNLKDQQQQMSLCPDTECLTVPPYKRDLYQKTKLRL 380

Db 475 SFMTCPILAVTQVNGLYDNRMSRRTVIL-----509

Qy 381 QELSQOQPAQHCRLEVSREIFES---YRQVMKMRPKDLWKLMLKFRGEGLDYGGV 437  
 Db 510 YSLVQGQNLNPYLRUKVRRHITDIALYRLEMAMENPADLKQKLYTFEGQVQDGGV 569

Qy 438 AREWYVJLSHEMLNPYGYGLFOYSRDDIYTLOQINPDSAVPEHLSYFHFVGRIMGAVFHG 497  
 Db 570 SKEFFQQLVVEBIRNEDIGHTYD-ESTKLFWENPSSP---ETEGQFLIGITVGLAYNN 625

GENERAL INFORMATION:  
 APPLICANT: Roife, Mark  
 APPLICANT: Eckstein, Jens W.  
 APPLICANT: Draetta, Giulio

DB 626 CILDVHFPMVYRKLMGKKGLFVTDGSHPVLYQSLSLDLERYGVNEDDMMITFQISQTN 685

555 AYGTEIQLKLNGKSIPVNEENKEVRYLTVNPRGLGIEAQFLALQKGNEYVTPHIL 614  
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 666 LPGNPMDYKLKGNDKIPITNREKFVNLYSDYLINKSVEKQFFAFRFGFHMVNTNESPL 745  
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 746 KYLRPPEIELLJCGSNLDFQALEETEYDGYYRDSVLREFEVVISFTDQQRFLF 805  
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 673 QFVYTGSSRVPLGG--FKALQGAAGPRLFTIHQIDACTNNLPAKHTCPNCNRIDIPPESYE 729  
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 730 KLYEKULITAETTCGFAY 747  
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 856 KLKERLIIKAITYAKGFKM 873  
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 CULT 15  
 08-767-942A-21  
 Sequence 21, Application US/08767942A  
 Patent No. 6061982  
 GENERAL INFORMATION:  
 APPLICANT: Roles, Mark  
 APPLICANT: Chiu, M. Isabel  
 APPLICANT: Berlin, Vivian  
 APPLICANT: Damagnez, Veronique  
 APPLICANT: Dratka, Giulio  
 APPLICANT: Guillaume, Cottarel  
 TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES  
 NUMBER OF SEQUENCES: 45  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109-2170  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/767,942A  
 FILING DATE: 17-DEC-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Vincent, Matthew P.  
 REGISTRATION NUMBER: 36,709  
 REFERENCE/DOCKET NUMBER: MIV-C29.04  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-832-1000  
 TELEFAX: 617-832-7000  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 874 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 08-767-942A-21  
 query Match 13.2%; Score 534.5; DB 3; Length 874;  
 est Local Similarity 25.1%; Pred. No. 4.9e+41; Gaps 23;  
 matches 185; Conservative 117; Mismatches 275; Indexes 161; Gaps 23;  
 105 NRLKDGYQRLDLCKLGPN---DDTDTGQIVVLSQESDRIGT-----GQVYDCS 152  
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 202 SRIGDSSQGDNLNQLQKQGPDDVSVDIAIR RVYTRLNLSEKIIATAFLNALVYLSPYVFC 260  
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 153 RLFDNDLDPGWEERPPASGRIQYINHITRTQWERPTRPASEYSSGRPLSCFVDENTPI 212  
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 213 SGTNG-----ATCGGSSDPRLAERRVRSRQRNRTMSRTH-----247

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Job time : 18.7634 secs

Gencore version 5.1.6											
Copyright (c) 1993 - 2004 Compugen Ltd.											
protein - protein search, using sw model											
on: February 20, 2004, 15:27:02 ; Search time 33.0523 Seconds (without alignments)											
Sequence: 1 MSNPGRRNPGPKLRLTVLC.....EKLYEKLTAIEETCGFAVE 748 4738.482 Million cell updates/sec											
file: US-10-009-945-4	effect score: 4038	seqs: 209382283 residues	real number of hits satisfying chosen parameters:	801455	Minimum DB seq length: 0	Maximum DB seq length: 2000000000	at-processing: Minimum Match 0% Maximum Match 100%	Listing first 45 summaries	Published Applications_AA: 1: /cnm2_6/podata/1/pubpa/pcru/0s07_pubcomb.pep: 2: /cnm2_6/podata/1/pubpa/pcru/0s07_new_pub.pep: 3: /cnm2_6/podata/1/pubpa/0s06_pubcomb.pep: 4: /cnm2_6/podata/1/pubpa/0s07_new_pub.pep: 5: /cnm2_6/podata/1/pubpa/0s07_new_pub.pep: 6: /cnm2_6/podata/1/pubpa/pcru/pubcomb.pep: 7: /cnm2_6/podata/1/pubpa/0s08_new_pub.pep: 8: /cnm2_6/podata/1/pubpa/0s08_pubcomb.pep: 9: /cnm2_6/podata/1/pubpa/0s09_pubcomb.pep: 10: /cnm2_6/podata/1/pubpa/0s09b_pubcomb.pep: 11: /cnm2_6/podata/1/pubpa/0s09c_pubcomb.pep: 12: /cnm2_6/podata/1/pubpa/0s09_new_pub.pep: 13: /cnm2_6/podata/1/pubpa/0s10_pubcomb.pep: 14: /cnm2_6/podata/1/pubpa/0s10b_pubcomb.pep: 15: /cnm2_6/podata/1/pubpa/0s10c_pubcomb.pep: 16: /cnm2_6/podata/1/pubpa/0s10_new_pub.pep: 17: /cnm2_6/podata/1/pubpa/0s60_new_pub.pep: 18: /cnm2_6/podata/1/pubpa/0s60_pubcomb.pep: US-10-021-660-81		
; Sequence 81, Appl ; Sequence 2, Appl ; Sequence 14, Appl ; Sequence 819, Appl ; Sequence 4, Appl ; Sequence 2966, Ap ; Sequence 816, Ap ; Sequence 279, App ; Sequence 126, App ; Sequence 277, App ; Sequence 15, App ; Sequence 9, App ; Sequence 275, App ; Sequence 6, App ; Sequence 312, App ; Sequence 32, App ; Sequence 31, App ; Sequence 16, App ; Sequence 249, App ; Sequence 46, App ; Sequence 11, App ; Sequence 13, App ; Sequence 32, App ; Sequence 31, App ; Sequence 16, App ; Sequence 25, App ; Sequence 25, App ; Sequence 5, App ; Sequence 157, App ; Sequence 16, App ; Sequence 1110, App ; Sequence 34, App ; Sequence 24, App ; Sequence 28, App ; Sequence 29, App ; Sequence 30, App ; Sequence 70, App ; Sequence 26, App ; Sequence 49, App											
ALIGNMENTS											
RESULT 1											
; Sequence 81, Application US/10021660 ; Publication No. US20030152926A1 ; GENERAL INFORMATION: ; APPLICANT: Murray, Richard ; APPLICANT: Glynn, Richard ; APPLICANT: Watson, Susan R. ; APPLICANT: EOS Biotechology, Inc. ; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis ; COMPOSITIONS AND METHODS OF SCREENING FOR ANGIOGENESIS ; TITLE OF INVENTION: Modulators ; FILE REFERENCE: 018501-000710US ; CURRENT APPLICATION NUMBER: US/10/0021_660 ; CURRENT FILING DATE: 2001-12-06 ; PRIORITY APPLICATION NUMBER: US/09/784,356 ; PRIORITY FILING DATE: 2001-02-14 ; PRIORITY APPLICATION NUMBER: US 09/637,977 ; PRIORITY FILING DATE: 2000-08-11 ; SOFTWARE: Fast-SEQ for Windows Version 3.0 ; SEQ ID NO: 81 ; LENGTH: 748 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-021-660-81											
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.											
SUMMARIES											
%											
Result No.	Score	Query Match	Length	DB ID	Description						
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2	3939.5	97.6	735	12	US-10-013-955-2						
3	3001	74.3	722	15	US-10-017-534-14						
4	2775	68.7	514	12	US-10-013-975-819						
5	1554	38.7	766	12	US-10-013-955-4						
6	1530.5	37.9	832	12	US-10-032-565-7296						
7	1453.5	36.0	869	15	US-10-012-714-8162						
8	1370.5	33.9	911	15	US-10-005-833-279						
9	1355.5	33.6	725	15	US-10-185-050-126						
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11	1354.5	33.5	927	15	US-10-097-534-15						
12	1353.5	33.5	995	15	US-10-097-334-9						
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Db	1	MSNPGRRNPGPKLRLTVLC.....EKLYEKLTAIEETCGFAVE	12	MSNPGRRNPGPKLRLTVLC.....EKLYEKLTAIEETCGFAVE	12	MSNPGRRNPGPKLRLTVLC.....EKLYEKLTAIEETCGFAVE					
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121 GPNNDTGYQIVVSLQRDRGTTGGQVVDCSRLLPDGMWBERTASGRIOYLNHIT 180  
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 181 RTTQWERTRPASEYSSPGRPLSFCFDTDENPISGTNGATGQSDDPRLAERRTSQRHRN 240  
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 241 YMSRTHLHTPPDLPEGYEQRTIQGGYFLIQTOTGVSTWHDPYRVLDSNINCEELGPLP 300  
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 301 PGWBEIRNTATGRVYFVDHNNRITQFDPRLSANLHLVLRNQNQLKDQQQQVYSLCPDPT 360  
 301 PGWBEIRNTATGRVYFVDHNNRITQFDPRLSANLHLVLRNQNQLKDQQQQVYSLCPDPT 360  
 361 ECLTVPRYKRDLYQKLKILRQLSQOOPAHCRCLEVSREEIFEFSYQVMKRPKDILWK 420  
 361 ECLTVPRYKRDLYQKLKILRQLSQOOPAHCRCLEVSREEIFEFSYQVMKMRPKDILWK 420  
 421 RLMIKFREBEGDLYGQAREWYLSSHEMINPYTYLQFOYSRDDITYLQINPDSAVNPHEL 480  
 421 RLMIKFREBEGDLYGQAREWYLSSHEMINPYTYLQFOYSRDDITYLQINPDSAVNPHEL 480  
 481 SYHFVGRIMGNAVFHGHYIPOGFTLPFYKOLGKSLTIDDMELVDPLHNSLWILEND 540  
 481 SYHFVGRIMGNAVFHGHYIPOGFTLPFYKOLGKSLTIDDMELVDPLHNSLWILEND 540  
 541 ITGVLDHTFCVHNAYGETIOHELKENGKSLPVRENKEYVPLYVNRFLRGIAQFLA 600  
 541 ITGVLDHTFCVHNAYGETIOHELKENGKSLPVRENKEYVPLYVNRFLRGIAQFLA 600  
 601 LQKGENEVIPQHLLKTDEKELELLIICLGSKIDNDWKNTRLKCTPDSNIVKWFVKAV 660  
 601 LQKGENEVIPQHLLKTDEKELELLIICLGSKIDNDWKNTRLKCTPDSNIVKWFVKAV 660  
 661 EPPDEERARLLQVTGSSRVPLOGKALOGAAGRFLTHQIDACTNNLPAKHTCFNRI 720  
 661 EPPDEERARLLQVTGSSRVPLOGKALOGAAGRFLTHQIDACTNNLPAKHTCFNRI 720  
 721 DIPPYESEKLYEKLLTAIEETCGFAVE 748  
 721 DIPPYESEKLYEKLLTAIEETCGFAVE 748

WUFT 2

Sequence 2, Application US/10313955-2  
 Publication No. US20030199056A1  
 GENERAL INFORMATION:  
 APPLICANT: Beach, David H.  
 Caliguri, Maureen  
 Nefsky, Bradley  
 TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109-1700  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/313,955  
 FILING DATE: 05-Dec-2002  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/09/392,163

FILING DATE: <Unknown>		
APPLICATION NUMBER: US 08/539,205		
FILING DATE: <Unknown>		
ATTORNEY/AGENT INFORMATION:		
NAME: Vincent, Matthew P.		
REGISTRATION NUMBER: 36.709		
REFERENCE/DOCKET NUMBER: CSV-005.0.1		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: (617) 832-1000		
TELEFAX: (617) 832-7000		
INFORMATION FOR SEQ ID NO: 2:		
SEQUENCE CHARACTERISTICS:		
LENGTH: 735 amino acids		
TYPE: amino acid		
TOPOLOGY: Linear		
MOLECULE TYPE: protein		
SEQUENCE DESCRIPTION: SEQ ID NO: 2:		
US-10-13-955-2		
Query Match	97.6%	
Best Local Similarity	98.0%	
Matches	733;	
Conservative	0;	
Mismatches	2;	
Indels	13;	
Gaps	1	
Qy	1	
1 MSNPGRRRNRPVKRLTIVLCAKNUVKKDFRLLDPFPKAIVYDGSQCHSTDTVKNTLDPK 60		
Db	1 MSNPGRRRNRPVKRLT-----GLPDPFAKVVNDGSGQCHSTDTVKNTLDPK 47	
Qy	61 WNWHDLYIKKSDSVTISWNHKKIHKKQGAFLGCYRLSNAINRLKDGTQRLDLCKL 120	
Db	48 WNWHDLYIKKSDSVTISWNHKKIHKKQGAFLGCYRLSNAINRLKDGTQRLDLCKL 107	
Qy	121 GPNDNDTVRGQIVVLSQSRDRIGTGQYVDCSLRFNDLDPDWEERRTASGRIQYLNHIT 180	
Db	108 GPNDNDTVRGQIVVLSQSRDRIGTGQVDDCSRLLFDNDLDPDWEERRTASGRIQYLNHIT 167	
Qy	181 RTTOWERPTPASESSPQRPLCFUDNTPISTGNGATCGSSDRLAERVRSGHRN 240	
Db	168 RTTOWERPTPASESSPQRPLCFUDNTPISTGNGATCGSSDRLAERVRSGHRN 227	
Qy	241 YMSRTHLHTPPDLBEGYERTTOGQYVFLHQQTGSTVWHDPRVPRLDSNTCELGPLP 300	
Db	228 YMSRTHLHTPPDLBEGYERTTOGQYVFLHQQTGSTVWHDPRVPRLDSNTCELGPLP 287	
Qy	301 PGWEIRNTATGRVYFVDHNRRQFTDPRLSANLHLVNRLNQLDKQQQQQVSVLCPDDT 360	
Db	288 PGWEIRNTATGRVYFVDHNRRQFTDPRLSANLHLVNRLNQLDKQQQQQVSVLCPDDT 347	
Qy	361 ECLEYPRYKDLVOKLKIRQELSQOAGHCIEYSREEFESYRQVKMRPKDLNK 420	
Db	348 ECLEYPRYKDLVOKLKIRQELSQOAGHCIEYSREEFESYRQVKMRPKDLNK 407	
Qy	421 RLMIFRGEBSGLDGGVAREWLVLISHMLNPVYGLQYSRDDITYLQINPDSANVPEHL 480	
Db	408 RLMIFRGEBSGLDGGVAREWLVLISHMLNPVYGLQYSRDDITYLQINPDSANVPEHL 467	
Qy	481 SYFFVGRIMGMAYVFRGHYIDGSSFLPFYKQIGKSITLDDMELVDPDLHNSLWVTLEND 540	
Db	468 SYFFVGRIMGMAYVFRGHYIDGFLPFYKQIGKSITLDDMELVDPDLHNSLWVTLEND 527	
Qy	541 ITGVLIDHTFCYEHMAYGETIQLHEKPKNSKIPVNENKEYKVLVYNWRFLGTRIAQFLA 600	
Db	528 ITGVGDHTFCYEHMAYGETIQLHEKPKNSKIPVNENKEYKVLVYNWRFLGTRIAQFLA 587	
Qy	601 LQKGPNEVIPQHLLKTDEKELELIICGLGKDVNDMKVNTRLKCTPDMSIVKRNFKAV 660	
Db	588 LQKGPNEVIPQHLLKTDEKELELIICGLGKDVNDMKVNTRLKCTPDMSIVKRNFKAV 647	
Qy	661 EFPDDEERRARLLQQTVGSSRVPLQGFALQGAGPRLFTIHQIDACTNNLPKAHTCENRI 720	
Db	648 EFPDDEERRARLLQQTVGSSRVPLQGFALQGAGPRLFTIHQIDACTNNLPKAHTCENRI 707	
Qy	721 DIPPYESYEKLKYLTTAETCGFAVE 748	

708 DIPPIESYEKLYBKILLPAIBETCGFAVE 735

D	353	RESULT 3	Db	506	WILENDITPVLDHTFCVERNAAFFGRILQHBLKPNGRNPVTBENKKEYVRLYVNNWRPMRG1	565
	3-10-037-534-14	Sequence 14, Application No. US/10097534	Qy	595	EAQFLALQKQGFNBIVPQHLLKTDEKEELBLIGLGLIDVNDWKVNTLKHTCPDSNIVK	654
	GENERAL INFORMATION:	PUBLICATOR: US 20030049607A1	Db	566	EAQFLALQKQGFNBIVPQHLLKTDEKEELBLIGLGLIDVNDWKVNTLKHTCPDSNIVK	625
	APPLICANT: GREENER, TSYIKA MOSKOWTZ, HAIM	Qy	655	WFWKAVEFFDEERARLIOFVGSSRVPLQGPALO -- GAAGPRLFTHOIDACTNNLP	711	
	APPLICANT: REISS, YUVAL	Db	626	WFWKAVEFFDEERARLIOFVGSSRVPLQGPALO -- GAAGPRLFTHOIDACTNNLP	685	
	APPLICANT: ALROY, IRIS	Qy	712	KAHTCNRIDIPPIESYEKLYEKLTAETCGFAVE 748		
	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL FILE REFERENCE: PLV-001.01	Db	686	KAHTCNRIDIPPIESYEKLYEKLTAETCGFAVE 722		
	CURRENT FILING DATE: 2002-03-12	RESULT 4				
	PRIOR FILING DATE: 2001-03-12		US-09-764-875-819			
	PRIOR FILING DATE: 2001-03-12		Sequence 819, Application US/09764875			
	PRIOR FILING DATE: 2001-07-31		Publication No. US20040018969A1			
	PRIOR FILING DATE: 2001-12-07		GENERAL INFORMATION:			
	NUMBER OF SEQ ID NOS: 71		APPLICANT: Rosen et al.			
	SEQ ID NO 14		TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
	TYPE: PRT		FILE REFERENCE: PU202			
	ORGANISM: Homo sapiens		CURRENT APPLICATION NUMBER: US/09/764,875			
	-10-097-534-14		CURRENT FILING DATE: 2001-01-17			
	Best Local Similarity 74.3%; Score 3001; DB 15; Length 722;		Prior application data removed - consult PALM or file wrapper			
	Matches 565; Conservative 74.6%; Pred. No. 3.1e-269; Mismatches 71; Indels 58; Gaps 8;		NUMBER OF SEQ ID NOS: 1449			
	12 VKLRLTYLCARNLVKKDFERPLDPAKVYVDGSCSCHSTDVTNNTLPKQHNDVYDYGK 71		SOFTWARE: PatentIn Ver. 2.0			
	4 IKRLRLTYCAKNLAKDFERPLDPAKIVVDGSCSCHSTDVTNNTLPKQHNDVYDYGK 63		SEQ ID NO 819			
	72 SDSVTISWVHKKIKHKQKAGELGGCVRLISNAITBLKDTGYQLDLCKLGPNDDVTRGQ 131		LENGTH: 514			
	64 TDSITISWVHKKIKHKQKAGELGGCVRLISNAISRLKDTGYQLDLCKLGPNDDVTRGQ 123		TYPE: PRT			
	132 IVVSLOSDRIGTGQVYDGSRLPFDLPGWEERRTASGRTQYLHITRITQWERPTRP 191		ORGANISM: Homo sapiens			
	124 IVVSLOSDRIGTGQVYDGSRLPFDLPGWEERRTASGRTQYLHITRITQWERPTRP 191		US-09-764-875-819			
	192 ASEYSPGRPLISCFYDENTPISGTGATCG-----QSSDPRLAERRVRSQRHNRN 242		Query Match	68.7%	Score 2775; DB 12; Length 514;	
	155 --EDDGPGRPLISCFMEEPAFTDSTGAAAGGGNCRFVESPQSDQRLQAQRLNPDVRGSL 212		Best Local Similarity	59.8%	Pred. No. 1.7e-248;	
	243 ---SPTHLATPPDLPDPEGYEQRTQOGQYFLHTQGTYSTWHPRFRDLSNSCDELGP 298		Matches	513;	Mismatches 0; Indels 0; Gaps 0;	
	213 QTPQRPFHGSPEPPEGYEQRTTQGQYFLHTQGTYSTWHPRFRDLSNSCDELGP 272		QY	235	SQRVNNTMSRTHHTPPDLPDPEGYEQRTTQGQYFLHTQGTYSTWHPRFRDLSNSC	294
	299 LPPGNEBIRNTATGRTYFYDHNRITQFTDPRLSANHVLQRNQKLDQQQQQVV--S 354		Db	1	SRRHRTMSRTHHTPPDLPDPEGYEQRTTQGQYFLHTQGTYSTWHPRFRDLSNSC	60
	273 LPPGNEVRSTVSGRYFVDRHNRITQFTDPRLSANHVLQRNQKLDQQQQQVV--S 354		QY	295	ELGPLPPOWEINTATGRTYFYDHNRITQFTDPRLSANHVLQRNQKLDQQQQQVV	354
	355 LCPDDTECLTYPRYKRDVLQKLKLQELSQQPQAGHCRIEVSEEEFPEESYQVMMDR 414		Db	61	ELGPLPPOWEINTATGRTYFYDHNRITQFTDPRLSANHVLQRNQKLDQQQQQVV	120
	329 L---EDBELPAQYRDLYQKLKVTRHELSLQQPQAGHCRIEVSEEEFPEESYQVMMDR 414		QY	355	LCPDDTECLTYPRYKRDVLQKLKLQELSQQPQAGHCRIEVSEEEFPEESYQVMMDR	414
	415 PKDLNKRMLIKERGEGLDYGSAVERWLYLISHEMINPQYGLFQYSRDLIYTQINPDSA 474		Db	121	LCPDDTECLTYPRYKRDVLQKLKLQELSQQPQAGHCRIEVSEEEFPEESYQVMMDR	180
	386 PKDLNKRMLIKERGEGLDYGSAVERWLYLISHEMINPQYGLFQYSRDLIYTQINPDSA 445		QY	415	PKLWKRMKLMIKERGEGLDYGSAVERWLYLISHEMINPQYGLFQYSRDLIYTQINPDSA	474
	475 VNPEHLSYFHFGYRINGMAYPHGHYDGGFTLPFKYOLIGKSITLDDMELVDDDLHNSLV 534		Db	181	PKLWKRMKLMIKERGEGLDYGSAVERWLYLISHEMINPQYGLFQYSRDLIYTQINPDSA	240
	446 INPDHSYFHFGYRINGMAYPHGHYDGGFTLPFKYOLIGKSITLDDMELVDDDLHNSLV 505		QY	475	VNPEHLSYFHFGYRINGMAYPHGHYDGGFTLPFKYOLIGKSITLDDMELVDDDLHNSLV	534
	535 WIENDITPVLDHTFCVERNAAFFGRILQHBLKPNGRNPVTBENKKEYVRLYVNNWRPMRG1 594		Db	301	WIENDITPVLDHTFCVERNAAFFGRILQHBLKPNGRNPVTBENKKEYVRLYVNNWRPMRG1	360
	329 L---EDBELPAQYRDLYQKLKVTRHELSLQQPQAGHCRIEVSEEEFPEESYQVMMDR 385		QY	595	EAQFLALQKGFNEVIBQHLLKXTFDKEELLIQGKIDVNDWKVNTLKHTCPDSNIVK	654
	415 PKDLNKRMLIKERGEGLDYGSAVERWLYLISHEMINPQYGLFQYSRDLIYTQINPDSA 474		Db	361	EAQFLALQKGFNEVIBQHLLKXTFDKEELLIQGKIDVNDWKVNTLKHTCPDSNIVK	420
	386 PKDLNKRMLIKERGEGLDYGSAVERWLYLISHEMINPQYGLFQYSRDLIYTQINPDSA 445		QY	655	WFWKAVEFFDEERARLQFVTGSSRVPLQGPALO -- GAAGPRLFTHOIDACTNNLPKAH	714
	475 VNPEHLSYFHFGYRINGMAYPHGHYDGGFTLPFKYOLIGKSITLDDMELVDDDLHNSLV 534		Db	421	WFWKAVEFFDEERARLQFVTGSSRVPLQGPALO -- GAAGPRLFTHOIDACTNNLPKAH	480
	446 INPDHSYFHFGYRINGMAYPHGHYDGGFTLPFKYOLIGKSITLDDMELVDDDLHNSLV 505		QY	715	TCTNRIDIPPIESYEKLYEKLTAETCGFAVE 748	
	535 WIENDITPVLDHTFCVERNAAFFGRILQHBLKPNGRNPVTBENKKEYVRLYVNNWRPMRG1 594		Db	481	TCTNRIDIPPIESYEKLYEKLTAETCGFAVE 514	

ISULT 5  
 :10-313-955-4  
 Sequence 4, Application US/10313955  
 Publication No. US20030199016A1  
 GENERAL INFORMATION:  
 APPLICANT: Beach, David H.  
 Caliguri, Maureen  
 Neffky, Bradley  
 TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 STREET: One Post Office Square  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109-2170  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/313,955  
 FILING DATE: 05-Dec-2002  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/09/392,163  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: US 08/539, 205  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Vincent, Matthew P.  
 REGISTRATION NUMBER: 36,709  
 REFERENCE/DOCKET NUMBER: CSV-005 .01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 832-1000  
 TELEFAX: (617) 832-7000  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 766 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 -10-313-955-4

Query Match 38.7%; Score 1564; DB 12; Length 766;  
 Best Local Similarity 41.1%; Pred. No. 9 4e-136; Indels 132; Gaps 18;  
 Matches 338; Conservative 121; Mismatches 232;

1 MSNPGRRNGPVKLRLTVLAKNLYKDFPRLPPFPKVVVDGGQCHSTDVKNLDPK 60  
 1 MSNSAQR---RIRVTIVADGLKTKDFRFPPFPVITVDB-QPHTTIAKKCLNPY 55

61 WNOHYDLYIGKS DSTVLSYVNHKKHHKOGAGELGGCVRLSNAINRKDGYQL--DLC 118  
 56 WNETFEVNVTDNSTAIQVEDQKKE-KKGQGFLGVNLRVGDVLDIAIGGDEMTRLK 114

119 KLGPNNDT VQGQVQVSLQ-----DL PDWEERTA SRIQYLNHTRTQ 184 .  
 115 K--SNENTVYHGKIIINLSTAOSTLQVPSAAASGARTORTSITNDPQSSSSVRNPA 172  
 138 -----SRDQIGGQQVQVDSRLDN-----DL PDWEERTA SRIQYLNHTRTQ 184 .  
 173 SSRAAGSPTRNAPASPARSERPTSSEDQYGRPLPPWERRTDNLRTYYDHNTSTT 232

185 WERTP----RPAISYSSPGRPLSCFVBDNTPAGTCCQSDDPRLARRYVSQRH 238  
 233 WIRPNSSVGAARAEHLSSAS-S SANTEGVQDSSSAA-----RRTEASVLT--- 279

239 RNMYSRTHLHTPPDLEPGYEQRTTQGQGYFLHTQTGASSNNIATITSGVNRLRGSA 292

Db 280 ---SNATTAGSSELPPCWEQYTPBGRPFYDHTRTTWWDPRRQQYRSYGGPNNT 335  
 Qy 293 ----CBEIGPLPGWEIRNTATGTYFVDINNRTIQFTDERLSANLHLYLNQNQLKDQ 347  
 Db 336 IQQOPVSQGPBLSGWEMRLLTNTARYFDENTKTWDDBRLPSSL-----DQ 384  
 Qy 348 QQQyvSISLCPDPECLTYPRYKDLVQKLILRQELSQQ--QPAQHCRIEVSEEEIFEE 405  
 Db 385 -----NPQYKRDFRKLIVY--LSQPALHPLEGQCHIKVRNHIFED 425  
 Qy 406 SYROVMKMRPKDOLWKRMKIKFGEEGLDYGSVAEMLYLISHEMLNPMLPYGLFOYSRDDY 465  
 Db 426 SYABIMROSATDILKURLMKIPDGDLYDGGCSREYFFLSHEMNPFCYCLEFVSSVDNY 485  
 Qy 466 TLQNPDSAVNPPLHSYFHVGIMMAVFGHYDGGFLIPYKOLGKSITLDDMELY 525  
 Db 486 TLQINPHESGINSNPPLHNTYFQKGRVIGLAIFFRYDFAFFVSYTMVILQCKVTLQDMESM 545  
 Qy 526 DPDLINSLWILENDINGVLDFCUEHMANVYI QHELKPGKSLIPABENKEVYRLV 585  
 Db 546 DAEYRSLWVILNDINGVLDFTSEDNCGEVVTIDLKPGNRIEVBENKEYVDLV 605  
 Qy 586 VNRNFLRGTEAQFLALQGENVTPQHLLKTFDEKELELLTGIGKIDYNDWKVNTRLKH 645  
 Db 606 TVW IQKRIEQQPNAFEGESLIPQELINVFDERPELLELIGGSEIDMEDWKHKDYS 664  
 Qy 646 CTTPSNITVWFWAKAVEFDEERARLQFQTSRPLQOFKAQGAAGERLFTHQIDA 705  
 Db 665 YSENDQIJKWFNWLMDWSNEKSKRLLQFQTGTSRIPVNGEKDLOGSDGERKFIERAGE 724  
 Qy 706 CTHNLPKAHTCFTRIDIPPYESYKLYEKULATAETTCGFAVE 748  
 Db 725 -PNKLPKAHTCFNRLLDPPYTSKQDJDHKLUSTAETTCGFAVE 766

RESULT 6  
 US-10-032-585-7296  
 ; Sequence 7296, Application US/10032585  
 ; Publication No. US2003018095A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Terry, Roemer D.  
 ; APPLICANT: Bo, Jiang  
 ; APPLICANT: Charles, Boone  
 ; APPLICANT: Howard, Bussey  
 ; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery  
 ; FILE REFERENCE: 10182-005-919  
 ; CURRENT APPLICATION NUMBER: US/10/032,585  
 ; CURRENT FILING DATE: 2001-12-20  
 ; NUMBER OF SEQ ID NOS: 000  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO: 7296  
 ; LENGTH: 832  
 ; TYPE: PRT  
 ; ORGANISM: Candida albicans  
 US-10-032-585-7296

Query Match 37.9%; Score 1530.5; DB 12; Length 832;  
 Best Local Similarity 38.4%; Pred. No. 1 4e-132;  
 Matches 338; Conservative 120; Mismatches 228; Indels 195; Gaps 21;

Qy 6 RRNGPYKLRLTVLCAKNLYKDFPFLPDPFAKYVYDGSQGCHESTDTVKNTLDPKMNQHY 65  
 Db 9 RSNNNTTINVKVAEESLYKRDVFRQDPBAVLTVDGS-QTKTTITAKTUNPYWNNTF 67

Qy 66 DLYIGKSDSV-TIISWNHKKHKGQAGELGCVR---LISNAINRLKDGTQYRLICK 119  
 Db 68 N-QAKEDSILVQFQKCF-KCDQGFGLGVINVRIGDVIDLSNSSETTR--DLRK 123

Qy 120 LGNDNDTGYQVIVSLQSRPRTGQVQVW----- 150

Db 124 --SNENLAVSGKXIVVI-SHNRNSNGGGVTTATRTGTGASSNNIATITSGVNRLRGSA 180

151 -----CSRFDN-- 157  
 181 TTANSTAOASSDATVGANGSGPTSSUPPLQGHDETAATPGGAGAAGAASTQYSSSED 240  
 158 ---DLPDWEEERTASRQIYLHITRTTOWERPTRPASE----- 194  
 241 QYGRLPPPOWERTTDNFERTTYDHDNSRTTWORPHQSETERSQQRQSETEAERQHRC 300  
 195 YSSPGR---PLSCFVDBNTPIISGTINGATCQSS-----DPLRAERRVSQHBN 240  
 301 RTIPGEVSVSPL----PTGSNISITSGNVTNAGANTPNPAAVSMASGATT 352  
 241 YNSRTHLHTPDLPEGYEQRTQQGYFLHTOTSYSTMHDPRYRDLNSNIN---- 292  
 353 GLG-----ELPSGWEQRPFTEGPYFYDHNTRTIVDPRQSYQTFGPNTTCQO 404  
 293 -CEELGLPLPPGMIBRINTATGEGYFYDHNARNTTOFDPLRSANLHLVLNRQNQLKDQQQQ 351  
 405 PVSQLGPJPSGMEMRLNTNTARYFVDHNTKTWTMDPRLPSSL-----DQ---- 449  
 352 VSLCPDPDTTECHLTYPKRDVLQKXKILRQBLSOQQP---AGRCHRIEVSRBIEEESY 407  
 450 -----NPVQYKRDFRKTYIYF----SOPALRILPQCHIKVRDHIFEDSY 492  
 408 RQVMRQRPDKLMKRMKTFREBGLDGGYAREWNYLSEMIAHYGLFOYSRSDIXYL 467  
 493 QBIMRQPDPEDLKRMKMFQSEGLDGGYSEREFPLSHDMTNPFYCFLFEISSHDNTL 552  
 468 QINPDSAVNPEELSYPHFVRIGMMAVPHGHYIDCGFTLPPFYKOLLGKSITLDDMELYDP 527  
 553 QINPNSGGINPEHLNWXPPIGRVGGVHFRFLDFFGALYKMLHKKVTLQDMBGYDA 612  
 528 DLHNSLYWILENDITGVLDTFTCVEHNAYGEIIOHELKGKSITIPVNRENKEBYVLYVN 587  
 613 EPTYSLXWILDITGVLDTLDFSAEESFBEIVDLSKGRDIEVTBENKHEYVLEITE 672  
 588 WRFLRGTEAQFLALQGENEYIPOHILKTSDEKELELICLGLGKIDNDWKUNTRIGHT 647  
 673 WRISKREVQPKAFIDGENELIPQILVNVDERELLLGLAELIDCDWKXHTDWRGYQ 732  
 648 PDSNITKWNWAVEFDEERARLLOFVTGTSRVPLQGPKALOGAAGRPLFTIHQDACT 707  
 733 ENDQVOMFWKNCINENDSEKARLQFQTGTGTSRIPVNGFKDQSGDPRRFTEKAGE-A 791  
 708 MNLPRAHTCFNDRIDTPYESYKUJBKLTAETCGFATE 748  
 792 NQLPKSHTCENRVDLPPYDTEYSLMKQLTLAVERTVGRGQB 832

SULT 7  
 -10-128-714-8162  
 Sequence 8162, Application US/10128714  
 GENERAL INFORMATION:  
 APPLICANT: Jiang, Bo  
 APPLICANT: Hu, Wengqi  
 APPLICANT: Tiskhoff, Daniel  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Broshkin, Alexey M  
 APPLICANT: Lemieux, Sébastien M  
 TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and Methods of Use  
 FILE REFERENCE: 10182-018-999  
 CURRENT APPLICATION NUMBER: US/10128714  
 CURRENT FILING DATE: 2003-04-13  
 PRIOR APPLICATION NUMBER: US 60/285, 697  
 PRIOR FILING DATE: 2001-04-23  
 PRIOR APPLICATION NUMBER: US 60/287, 066  
 PRIOR FILING DATE: 2001-04-27  
 PRIOR APPLICATION NUMBER: US 60/295, 890  
 PRIOR FILING DATE: 2001-06-05  
 PRIOR APPLICATION NUMBER: US 60/303, 899  
 PRIOR FILING DATE: 2001-07-09

151 -----CSRFDN-- 157  
 181 TTANSTAOASSDATVGANGSGPTSSUPPLQGHDETAATPGGAGAAGAASTQYSSSED 240  
 158 ---DLPDWEEERTASRQIYLHITRTTOWERPTRPASE----- 194  
 241 QYGRLPPPOWERTTDNFERTTYDHDNSRTTWORPHQSETERSQQRQSETEAERQHRC 300  
 195 YSSPGR---PLSCFVDBNTPIISGTINGATCQSS-----DPLRAERRVSQHBN 240  
 301 RTIPGEVSVSPL----PTGSNISITSGNVTNAGANTPNPAAVSMASGATT 352  
 241 YNSRTHLHTPDLPEGYEQRTQQGYFLHTOTSYSTMHDPRYRDLNSNIN---- 292  
 353 GLG-----ELPSGWEQRPFTEGPYFYDHNTRTIVDPRQSYQTFGPNTTCQO 404  
 293 -CEELGLPLPPGMIBRINTATGEGYFYDHNARNTTOFDPLRSANLHLVLNRQNQLKDQQQQ 351  
 405 PVSQLGPJPSGMEMRLNTNTARYFVDHNTKTWTMDPRLPSSL-----DQ---- 449  
 352 VSLCPDPDTTECHLTYPKRDVLQKXKILRQBLSOQQP---AGRCHRIEVSRBIEEESY 407  
 450 -----NPVQYKRDFRKTYIYF----SOPALRILPQCHIKVRDHIFEDSY 492  
 408 RQVMRQRPDKLMKRMKTFREBGLDGGYAREWNYLSEMIAHYGLFOYSRSDIXYL 467  
 493 QBIMRQPDPEDLKRMKMFQSEGLDGGYSEREFPLSHDMTNPFYCFLFEISSHDNTL 552  
 468 QINPDSAVNPEELSYPHFVRIGMMAVPHGHYIDCGFTLPPFYKOLLGKSITLDDMELYDP 527  
 553 QINPNSGGINPEHLNWXPPIGRVGGVHFRFLDFFGALYKMLHKKVTLQDMBGYDA 612  
 528 DLHNSLYWILENDITGVLDTFTCVEHNAYGEIIOHELKGKSITIPVNRENKEBYVLYVN 587  
 613 EPTYSLXWILDITGVLDTLDFSAEESFBEIVDLSKGRDIEVTBENKHEYVLEITE 672  
 588 WRFLRGTEAQFLALQGENEYIPOHILKTSDEKELELICLGLGKIDNDWKUNTRIGHT 647  
 673 WRISKREVQPKAFIDGENELIPQILVNVDERELLLGLAELIDCDWKXHTDWRGYQ 732  
 648 PDSNITKWNWAVEFDEERARLLOFVTGTSRVPLQGPKALOGAAGRPLFTIHQDACT 707  
 733 ENDQVOMFWKNCINENDSEKARLQFQTGTGTSRIPVNGFKDQSGDPRRFTEKAGE-A 791  
 708 MNLPRAHTCFNDRIDTPYESYKUJBKLTAETCGFATE 748  
 792 NQLPKSHTCENRVDLPPYDTEYSLMKQLTLAVERTVGRGQB 832

Query Match Score 1453.5; DB 15; Length 869;  
 Best Local Similarity 36.2%; Prod. No. 2.1-e-125;  
 Matches 332; Conservative 114; Mismatches 229; Index 243; Gaps 21;

QY 11 PKVLRU-TVUCAGNUVKDDEPR-----LPPDFAKTVVUDSGQCH 48  
 Db 15 PASSRLCRVTAADLQYKEDVFRKSYTIAILYVRLTSGAFAGFPDFAVATVGB-E-QTH 73  
 Qy 49 STDVTKNTLDPKRNQHNDLYIGKSDSVTISVNHKCIHKKGAGFJUCVRL----- 100  
 Db 74 TSVYKKTLPNPNMPEWRYVNDSTLAIQFDCQKF-KKDQGEGVINVPRGVDYDILQ 132  
 Qy 101 -----SNAINFNLK-----DTGYORLDDLCKLGPNDNTDTRGQIVVSL----- 136  
 Db 133 MGGDGESLPIRHSCDVSPLTFLILLTEMLTRDLKK---SNDNLVYVHGKLLINLSTNLST 190  
 Qy 137 -----QSARDRIGTGCQYDSCS----- 152  
 Db 191 PNTNQANGLHRSHTYQSSTTSQGVPQVAPSSSSHPAAGTAPVDPASNPSLNQRPVPSTR 250  
 Qy 153 -----RFLFDND-----LFDGWEERRATASGRQIQLNHTTRTQ 184  
 Db 251 PSCSTAAPASAAGAVNSHGSNTNLSSFDSSGRGLPAGWERDINGTYVDDINTRTT 310  
 Qy 185 WERTPRPASESSSPGRPLSCPYDENTPISGTINGATGQSSDPPLAERRVRSQRHRYM----- 242  
 Db 311 W---TRPSSNNYHAQ-----RSQREANMOUERRHQASRMLP 344  
 Qy 243 -----SRTLHHTPP-----DPLGEGYQORTQGQVY 268  
 Db 345 EDTGTGANSNLPSSQCAHTPPAGGSANAVSMMATGATTAGTAGELPPGWQRTTEGRPY 404  
 Qy 269 FLHTQGTVSTWHEDRPRVPLD---SNIN-----CBELGLPLPPGMEIRNTPATGRVY 314  
 Db 405 FVDINTTETTWDPRRQQTAMYQONANGNTTIIQOQPSQLGPLPSGMWMLNTARY 464  
 Qy 315 FVDINNRRTQFTPRLSANLHLVLRNQNOLQDQQQQVVSCLCPDDETECLTVPRYKRDLYQ 374  
 Db 465 FVDINTKTITWDPRFSSL-----DQ-----DQ-----GVPKQRDFRR 497  
 Qy 375 KUKLROBLSOOP-----OAGHRIBEVSYRBEFEESYRQYKMRPKDLNKRLMKFGRGE 430  
 Db 498 KLWYFR----SPADRLMSGCCHVTRNNIFEDSYAEINRQASDLCKRLMKFDFGED 552  
 Qy 431 GLDYGGVAREWLYLHSHEMLNPYGLFOYSRDDIYTQINPDSAVNPEHLSYFFVGRIM 490  
 Db 553 GLDYGGLSGEFFLSSHEMFYFCYKOMLKKVSLQDMEGYDTEFLHRNTWTWNDNDIEGTLELTS 672  
 Qy 551 VENAYGEIQLQHBLPKNGKS1PVNEENKEYYVRLVNVWFLRGIBAQFLALQGFNEYIP 610  
 Db 673 VDEKEGERRTIDLKFGGRDPVTNENKAEVRLVTEQFVAFMSFNELLIP 732  
 Qy 611 QHLLKTDFDEKELBLILICLGLKIDNDWKNTTRLKHCTPDSNIVKRMWKAEFFEBERRAR 670  
 Db 733 ADLWNVDFEREELLLIGGIADIDDDWKRHTDPRQYQESDEVIONFWKLVRSWAEQKSR 792  
 Qy 671 LIQFVOTSVRPLQGEFALOGAAGRPLFTHQIADACTNLPKAFTCENRIDPYESYK 730  
 Db 793 LUJFTGTSRIPVNGFKDQGSDPRTK-SGDPAAPLPSRTGFRNLDLPPYKSYET 851

731 LYERKLLTAIEETCGFAVE 748  
 , 852 LEHKMSTIAVEETLGFQEB 869

RESULT 8  
 Sequence 279, Application US/10205823  
 Publication No. US/0030108963A1  
 GENERAL INFORMATION:  
 APPLICANT: Schlegel, Robert  
 APPLICANT: Endgege, Wilson E.  
 APPLICANT: Ganna-arapu, Manjula  
 APPLICANT: Gorbatcheva, Bella  
 APPLICANT: Hoersch, Sebastian  
 APPLICANT: Kamatkar, Shubhangi  
 APPLICANT: Nonsey, Angela M.  
 APPLICANT: Glatt, Karen  
 APPLICANT: Zhao, Xumei  
 APPLICANT: Anderson, Dustin  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF PROSTATE CANCER  
 FILE REFERENCE: MRI-044  
 CURRENT APPLICATION NUMBER: US/10/205, 823  
 CURRENT FILING DATE: 2002-07-25  
 PRIOR APPLICATION NUMBER: 60/301, 982  
 PRIOR FILING DATE: 2001-07-25  
 PRIOR APPLICATION NUMBER: 60/314, 356  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/325, 020  
 PRIOR FILING DATE: 2001-09-25  
 PRIOR APPLICATION NUMBER: 60/341, 746  
 PRIOR FILING DATE: 2001-12-12  
 PRIOR APPLICATION NUMBER: 60/362, 158  
 PRIOR FILING DATE: 2002-03-05  
 NUMBER OF SEQ ID NOS: 455  
 SOFTWARE: FastSEQ for Windows version 4.0  
 SEQ ID NO 279  
 LENGTH: 911  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 -10-205-823-279

Query Match 33 9%; Score 1370.5; DB 15; Length 911;  
 Best Local Similarity 36.7%; Pred. No. 1.2e-117; Mismatches 234; Indels 207; Gaps 28;

Matches 324; Conservative 119; Mi smatches 234;

24 LYTKDFPRLP--DPFAKY--YVYNGQCH--STDYKNTLDPKNNOHYDLYIGKSD-S 74  
 69 LPTSDELFLPOTCDPPVKLSVYVALENRELAVTKTKTLPKNEEFYTRVNSNHR 128  
 75 VTI\$VNNHKKHHKKQGAGELGCVR-----LISNAINRLDTGY 112  
 129 LLFEVDFENRLTRDD--FLGQVDPVLPSHLPLTEDPTMERPYTFKDELLPRSHKSRYKGF 185  
 113 QBDLCKLGPMNDTFRGQIVVLSRDRGFTGTGQQVUDCSRLFDND-----L 159  
 186 LRLKAYMPXNG----GDBENSQRDMEHGMEVVD----SNDASASQOBELPPPL 235  
 160 PDGWEERITASGRIVQNLHTRTCTOWERPT-----RPA 192  
 236 PFGWKEVKDNGTYYVNNHNRTHRSIMDVISSESDDNTRQINQBAAHRRFRRH1 295  
 193 SEYSSP-----GRPLSCFVDENTPIGSTN-----GATCGOSSDPR-LAE--RR 232  
 296 SEDLEBEPSEGGDVDEPWET-ISEEVNNIGDSCLALPPPASPGRTSPOELSELRSRR 354  
 233 VR-----SQRHRNMSRTHL-----HTPPD-----252  
 355 LQTIPDSNGEOFSSSLTQREBSSRURCSVTDVAEQQHJPGAKDSBVRRAVKTDSNPQ 414

253 ---IPEGYEORTTQQGVYFLHTQTGVSTWHDRVP---RD 287  
 , 415 SPQSPYNSPKPKOHKVTOVSFLPQGWENIAPNGRPFIDNTKTWTEDRKLKFVHMR 474  
 288 LSNNINCBLGPPLPGWEIRNTATGRYFVDHNNRTOQFTDPLSANLHLVNRNQNLKDO 347  
 475 KTSLNPNDLGPPLPGWEERIHLLGRTYVIDANSKIQWEDRPL-----ON---- 519  
 348 QQQQVSLCPDDTCBLTPR--YKRLVQKLKILRQLSQQPQAGHCRLEVSRBEEFEE 405  
 520 -----PAITGPAVYSREFQKDYFRKLKTPADIPNRFEMKLHRRNIFEE 566  
 406 SYROMWOKRPDKW-RUMIKFRGEESGLDYGARWMLYLSHEMNPYGTFLQYSRDDI 464  
 567 SYRIMMSVKRPDVJKAHLWIEPESEGLDYGVARWMPFLSKEMNPYGLFSETDN 626  
 465 YTLQINPDSAV-NPEHLSYFHFGWGRIMGAVFHGHYIDGGFTLPPYKOLIGKSTLDDME 523  
 627 YTLQINPNSGLCNDHLSYFTFIGRVAGLAVFHKGKLDGFIRPFYKOMLGQQTLMDE 686  
 524 LYDDDLERSLWVLENDUTGVLQDHTCVERHAYGETQHKLKPDKDEKEBLIICLGKIDVNDNKVNTRL 643  
 687 SVSBYNSLKLWLENDPT-BUDMFCEIDENFQDVLKRNSEIMTNKREYID 745  
 584 LYNNWRERGIEAQFLAQKGENEVIPQHLLKTDEKEBLIICLGKIDVNDNKVNTRL 643  
 746 LVVWRFPRVNRVOQMNALFEGTEPLIDLKIFDNEELLMCGLGVDYNDRQHSY 805  
 644 K--HCTPDSNIVKWMKAVEFDEERRARLQFVTGSSRYPLOGFKALQAGAAGRFLTH 701  
 806 KNQYC-PNHPVQIWQEWCAVLLMDAECRILQFVGTGTSRVPMNQGFAELYGSNGNQPLFITE 864  
 702 QIDACTNLPRKATCFNRIDIPYESEKLYKLTAIEETCGF 745  
 865 QWGS-PEKIPRHTCPNRLDLPPYEFEDIREKLLMAVENAQGF 907

RESULT 9  
 US-10-185-050-126  
 ; Sequence 126, Application US/10185050  
 ; Publication No. US20030077577A1  
 ; GENERAL INFORMATION:  
 ; CORRESPONDENCE ADDRESS:  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/185, 050  
 ; FILING DATE: 28-Jun-2002  
 ; CLASIFICATION: <Unknown>  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/826, 516  
 ; FILING DATE: 03-Apr-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MISROCK, S. LESLIE  
 ; REGISTRATION NUMBER: 16, 872  
 ; REFERENCE/DOCKET NUMBER: 1101-208-999  
 ; TELECOMMUNICATION INFORMATION:





; TYPE: PRP  
; ORGANISM: Homo sapiens  
; US-10-205-823-275

Query Match 33.5%; Score 1353.5; DB 15; Length 995;  
Best Local Similarity 44.6%; Prod. No. 5.Ie-116;  
Matches 188; Indels 60; Gaps 12;  
Matches 275; Conservative 93; Mismatches 188;

QY 159 LPDSEWEERTASRRIQIYINHTRTOWERUTPRAEYSSPG-----RPLS 203  
Db 407 LPSSWEERKDAKGRTTYVHNHNRRTTTRPMQLAEGASGSATSNMHLIEPQIRPRPS 466

QY 204 C--FVDNTPIISGTGNGATCGSSDPRLAERRRSQRHRNTMSRTHLHTPPDLPEGYEAR 260  
Db 467 LSSPTVTISAPLEGAKSPVRRAVKOTLNSPQSPSPYNSPKHQKVTSFLPPGMEMR 526

QY 261 TTOGQOYYFLHTOTGVSTWHDPRVP----RDLNINCEGLPLPGWEIRNTATGRVYF 315  
Db 527 IAPNGRPPIFDANTKTTIWEDPLRKPFVHRSKTSINPNPDGZPLPGWEIRTHLDERTFY 586

QY 316 VDHNNRRTQFTDPRLSANLHVLRNQNOLKDQQQQVVSCLCPDDTECLTVPR--YKRDVL 373  
Db 587 IDEINSKTTQWEDPL-----ON-----PAITGAVPVPSREFK 618

QY 374 OKUKLROELSQOOPQRCHEVSRBEEFESYRQVMKMPKDLWK-RLMIKFRGREGL 432  
Db 619 QKDYDFRKCKKPADIEPNRFEMKLHNNFEEBSYRIMSVRDPVLKARLNTTEFSBKGL 678

QY 433 DYCQVAREBWLILSHMLNPYGLFOYSRDIYTLQINPDSAV-NPEHLSYFHVGRTM 491  
Db 679 DYGQVAREBWLILSHMLNPYGLFOYSRDIYTLQINPDSAV-NPEHLSYFHVGRTM 491

QY 492 MAYFHGHYIDGGFTLPYKQOLIGKSITLDMELVDPDLANSLLWILENDLTGVDLDTHTFCV 551  
Db 739 LAVFHGKLQDFFIRPFYKOMLGKQITLNDMEVSDEYNNLSLKWILENDFT-ELDMFCJ 797

QY 552 EHNAQGBIIQHQLKPGNSITPNEENKETVRLYNNWRFLRGTEAQLAQGFNFNEVIFQ 611  
Db 798 DEENFGCTYQVDLKPGNSEIMVTNENKREYIDLVQWRFNVRQKOMNAFLEGFTELLPI 857

QY 612 HLLKTTPDEKELELLIICGLKIDVNDKVNTRLK-HCTPDSNTYTKWFKAVEFDEERA 659  
Db 858 DLIKVTDENEELLMGGLDVDNDVRQHSTYKNGYC-PNHPVQWNAVLMDAEKKI 916

QY 670 RLQFYTGSRVPLQGFKALOGAAGPRLFTTHQIDACTNNLPAKHTCENRIDIPRYEYE 729  
Db 917 RLQFYTGSRVPLQGFKALOGAAGPRLFTTHQIDACTNNLPAKHTCENRIDIPRYEYE 975

QY 730 KLYEKULTAIETCTGF 745  
Db 976 DIREKCLMAVENAAQGF 991

QY 910-205-823-275  
Db 991 Application US/10205823  
; CURRENT APPLICATION NUMBER: US20030108963A1  
; PRIORITY INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Endee, Wilson O.  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Gorbatcheva, Bella  
; APPLICANT: Hoerlich, Sebastian  
; APPLICANT: Kamakkar, Shubhangi  
; APPLICANT: Wonsley, Angela M.  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Anderson, Dustin  
; APPLICANT: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; APPLICANT: NOVEL GENES, COMPOSITIONS, KITS, AND  
; APPLICANT: THERAPY OF PROSTATE CANCER  
; APPLICANT: Prior Filing Date: 2001-07-05  
; APPLICANT: Prior Application Number: 60/314,356  
; APPLICANT: Prior Filing Date: 2001-08-22  
; APPLICANT: Prior Application Number: 60/325,020  
; APPLICANT: Prior Filing Date: 2001-09-25  
; APPLICANT: Prior Application Number: 60/341,746  
; APPLICANT: Prior Filing Date: 2001-12-12  
; APPLICANT: Prior Application Number: 60/362,158  
; APPLICANT: Prior Filing Date: 2002-03-05  
; APPLICANT: SEQ ID NOS: 455  
; APPLICANT: ID NO: 455  
; APPLICANT: SOFTWARE: FastSEQ for Windows Version 4.0  
; APPLICANT: LENGTH: 995

RESULT 14  
US-10-313-955-6  
; Sequence 6, Application US/10313955  
; Publication No. US20030199036A1  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; CALIGURI, Maureen  
; NEIBBY, Bradley  
; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELION LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; MEDICAL TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/313, 955  
 FILING DATE: 05-Dec-2002  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/392,163  
 FILING DATE: Unknown  
 APPLICATION NUMBER: US 08/539,205  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Vincent, Matthew P.  
 REGISTRATION NUMBER: 36,709  
 REFERENCE/DOCKET NUMBER: CSV-005.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 832-1000  
 TELEFAX: (617) 832-7000  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 834 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 10-313-955-6  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 10-313-955-6  
 Query Match Score 1353; DB 12; Length 834;  
 best Local Similarity 44.6%; Pred. No. 4.e-16;  
 matches 275; Conservative 93; Mismatches 188; Indels 60; Gaps 12;  
 306 LSSPTVILSAPLEGADSPYRAVKTLNSPQSPQSPNPKHQVKTQSFLPPGEMR 365  
 261 TPGQQVYPLHTQTG/STWHPRPV----RDLNTINCEBGLPQGMWBIRNTATGRVYF 315  
 366 IAPNGRPFIDHNTKTTTWEPRLKPEVNRSKTSLNPDGLGPQGPHEERHLDGTFY 425  
 316 VDHNRRTQFTDPLSANLHLVLNRONOLKDQQQQQVVSLCPDDTECLTYPR-YKDLV 373  
 426 IDHNSKTQMDPRL-----ON-----PAITGPAYPSREFK 457  
 374 QKLKIRQELSQQPQAGHCIEVSREBEEESTRQMMRKPDLWKRMLKPRGBEGI 432  
 458 QKDYFRRKLKPCKADLPNRFNPKLHNNTNESTRIMVKRPLVYLWIEPESSXGL 517  
 433 DGGVAEYWLVLSHMLNPYGLFOYSRDEDTYLQINSDSAV-NPEHLSYFFVGIMG 491  
 518 DGGVAEYWLFULLSKMENPYPGLFOYSRDEDTYLQINSDSAV-NPEHLSYFFVGIMG 577  
 492 MAVFHGHYIDGGFTLDPYKQLLGKSTLDDMELVDPLHNSWLENDITGVLDHDFFCV 551  
 578 LAVFGCRKLGDGFIREFYKMLGQTLNDMEVSEYNSLWILENDPT-ELDMPC1 636  
 552 EHNAYGEJ1QHALKPGKS1PVNEENIKKEYVRLVYNWRLLRGTEAOFALQGNEVTPQ 611  
 637 DEENFGTGYQDLPKPGNSEMTVNENKREYD1VWQRQAS1YKNGC-1NHPY1QWFKAVLMDAKRI 696  
 612 HLLKTFDEKELELIICGLKIDVNDWKNTPLK--HCTPDSNIVKWFWKAYEFFDBERRA 669  
 697 DLKTFDENEELLLM:GLGDVNDWKNTPLK-1QHBLKPNGKS1PYUNENKKEYV- 755  
 670 RLIQFTGSSRYPLQGFKALOGAAGRPLFTHQDACTNLPKAHTCPNDRIPYVESYE 729  
 756 RLIQFTGTSRVPMNGPAELYSNGNQLETFTEQNS-PKPLPRAHTCFNRLDLPYETFE 814  
 730 KLYEKLTIAEETCGF 745  
 815 DLREKLMAVENAQGP 830  
 394 YTIQINPISAVNPEHLSYFHVGIMGMAVPHGHYIDGGFTLDPYKQLLGKSTLDDMEL 524  
 405 ESTRQVMNMRPKD1WKRMLIKFRGEEGLDYGCAREWLYLISHMENLPYGLFOYSRDDI 464  
 395 DSXZEMIQSASDLKRMK1KFEDGLDYGGLSERFFFLSHENFNPFYCLFEYSAHDN 454  
 465 YTQINPISAVNPEHLSYFHVGIMGMAVPHGHYIDGGFTLDPYKQLLGKSTLDDMEL 514  
 455 YTQINPISAVNPEHLSYFHVGIMGMAVPHGHYIDGGFTLDPYKQLLGKSTLDDMEL 514  
 525 VDPLHNSLWVLLENDITGVLDHFTCYENRAYGEJ1QHBLKPNGKS1PYUNENKKEYV- 582  
 515 VDPLHNSLWVLLENDITGVLDHFTCYENRAYGEJ1QHBLKPNGKS1PYUNENKKEYV- 574  
 583 -----RLYVWWRFLRGIEAFLALQKGFNENVIPOHLLKTFDKEBL 622

575 YLPLPLAEDDDKLTNGEPRLVTEWKIVKRVEEQENAFMSGENEELPADLYNVEBEREL 634  
623 ELLICCLGKDNDPKVNPRLKHCTPDSNIUVKFWKAVEFDEBRARLLQVTGSSRVP 682  
635 ELLICGTAIDDDKRFHDYRGYESDEVIONFWKIVRSWDAEOKSRLLQFTTGSSRIP 694  
683 LQGFKALOGAAGPRAFTIHOIADACTNLPKAHTCFNRDIPPESYEKLYEKULLTIEET 742  
695 VNGFDLQGDGPRFTIEK-SGDPPAALPKSHTCFNRLDLPYKSTETLERHKMSIAVEET 753  
743 CGFAVE 748  
754 LGFGQE 759

GenCore version 5.1.6  
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1 protein - protein search, using sw model

in on: February 20, 2004, 15:25:26 ; Search time 17.7974 Seconds  
 (without alignment)  
 4041.832 Million cell updates/sec

title: US-10-009-945-4  
 perfect score: 4038  
 sequence: 1 MSHPGRERRNGPVKLRLTVLC.....EKLYEKLTLAIEETCGFAVE 748

oring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

searched:

total number of hits satisfying chosen parameters: 283308

minimum DB seq length: 0  
 maximum DB seq length: 2000000000

est-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

atabase : PIR:76-\*  
 1: Pir1:  
 2: Pir2:  
 3: Pir3:  
 4: Pir4:  
 A: Tolerance of low pH in Schizosaccharomyces pombe requires a functioning publ

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1585.5	39.3	767	2 T37545	ubiquitin-protein
2	1564	38.7	766	1 S66562	probable ubiquitin
3	1521	37.7	815	2 T49744	probable ubiquitin
4	1484	36.8	809	1 S43217	ubiquitin-protein
5	1418	35.1	786	2 T39585	ubiquitin protein
6	1364.5	33.8	820	2 T46412	ubiquitin-protein
7	1355.5	33.6	887	2 S70642	ubiquitin ligase N
8	1177	29.1	708	2 I93195	NEDD4 ORF_2 - mouse
9	1044.5	25.9	671	2 T37900	probable ubiquitin
10	858	21.2	3227	2 T37964	probable ubiquitin
11	846.5	21.0	3839	2 T49793	related to TOM1 pr
12	805.5	19.9	1126	2 T01491	ubiquitin-protein
13	803	19.9	4056	2 H96599	protein Fl416_10
14	789	19.5	3268	2 S69625	hypothetical prote
15	709.5	17.6	889	2 T20274	hypothetical prote
16	626	15.5	310	2 T152646	DNA binding prote
17	596	14.8	221	2 T51886	hypothetical prote
18	534.5	13.2	874	2 A38920	B6 associated prot
19	465	11.5	807	2 T40821	probable ubiquitin
20	460.5	11.4	892	2 S57055	polyubiquitin-like
21	454	11.2	873	2 H85134	hypothetical prote
22	449	11.1	1142	2 T46155	hypothetical prote
23	445.5	11.0	1054	2 B38919	hypothetical prote
24	441.5	11.0	1083	2 T38951	probable ubiquitin
25	419.5	10.4	1029	2 S71752	Giant protein p619
26	407.5	10.1	4861	2 T26753	hypothetical prote
27	403.5	10.0	1066	2 T20373	hypothetical prote
28	387	9.6	1001	2 T20373	herc2 protein - mo
29	371	9.2	4836	2 T14346	

#### ALIGNMENTS

RESULT 1	T37545	ubiquitin-protein ligase (EC 6.3.2.19) publ [validated] - fission yeast (Schizosaccharomyces pombe)
N:Alternate names: ubiquitin ligase Publ		
C:Species: Schizosaccharomyces pombe		
C:Accession: T37545; T46555		#sequence_change 03-Jun-2002
R:McClue, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.		C:Date: 03-Dec-1993
R:Sakai, R.; Jia, Z.; Kargiannis, J.; Young, P.G.		A:Experimental source: Strain 972h - cosmid c1G7
Mol. Gen. Gent. 254, 520-528, 1997		A:Reference number: 221722
A:Title: Tolerance of low pH in Schizosaccharomyces pombe requires a functioning publ		A:Accession: T37545
A:Status: Preliminary; translated from GB/EMBL/DDJB		A:Status: Preliminary; translated from GB/EMBL/DDJB
A:Molecule type: DNA		A:Molecule type: DNA
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A:Cross-references: EMBL:Z99161; PIDN:CA16207_1; SPDB:GN00066; SPDB:SPAC11G7_02		A:Cross-references: EMBL:Z99161; PIDN:CA16207_1; SPDB:GN00066; SPDB:SPAC11G7_02
A:Experimental source: strain 972h - cosmid c1G7		A:Experimental source: strain 972h - cosmid c1G7
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A:Map position: 1		A:Map position: 1
A:Introns: 6/2; 14/1; 62/2		A:Introns: 6/2; 14/1; 62/2
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A:Description: involved in of the mitotic activating tyrosine phosphatase cdcc5 [valic		A:Description: involved in of the mitotic activating tyrosine phosphatase cdcc5 [valic
C:Superfamily: yeast ubiquitin-protein ligase; WW repeat homology		C:Superfamily: yeast ubiquitin-protein ligase; WW repeat homology
F:205-242/Domain: WW repeat homology <WW1>		F:205-242/Domain: WW repeat homology <WW1>
F:288-325/Domain: WW repeat homology <WW2>		F:288-325/Domain: WW repeat homology <WW2>
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Best Local Similarity 41.3%; Pred. No. 1e-100;		Best Local Similarity 41.3%; Pred. No. 1e-100;
Matches 340; Conservative 121; Mismatches 231; Indels 131; Gaps 17;		Matches 340; Conservative 121; Mismatches 231; Indels 131; Gaps 17;
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Db 1 MNSAQASR---KIRVTVAADGLYKRDVPPFPDPAVLVDGE-QTHTTAIAKTLNPY 55		Db 1 MNSAQASR---KIRVTVAADGLYKRDVPPFPDPAVLVDGE-QTHTTAIAKTLNPY 55
Qy 61 WNHQHYDLVIGKSOSVTSVWNEKIKHKKQAGFLGVRLLSNATNLKDTGYQRD--DLC 118		Qy 61 WNHQHYDLVIGKSOSVTSVWNEKIKHKKQAGFLGVRLLSNATNLKDTGYQRD--DLC 118

56 WNETFEYAVNDSTIAIQVFDQKKF - KKKGGQFLGVINLRGVDLAIQGDEMILTRDLK 114  
 119 KLGNDINDTURQIIVLSQ----- 137  
 115 K -SNEYTVHESKIIINSLSTAOSTLQVPSAAASGARTQTSITNDPQSQQSSVRNPA 172  
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 173 SSGAGSPRDNAPAASPASSEPRPTSFSEDDQYGRPPGHERRTNGTYVHNTTRT 232  
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 385 -----NVPOQTKRDPLPRKLIFY---LSQPALHPLPGOCHIKYVRNHFED 425  
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 706 CTNNLPAHHTCPNRIDPPIYESZELKYEKULTAETCTGPAVE 748  
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:SULT 2  
 ubiquitin-protein ligase (EC 6.3.2.19) - fission yeast (*Schizosaccharomyces pombe*)  
 Alternate name: E6-AP-like protein ubiquitin ligase  
 Species: *Schizosaccharomyces pombe*  
 Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
 Accession: S66562; PMID:8635463  
 Accession: S66562  
 Status: preliminary; nucleic acid sequence not shown  
 Molecule type: mRNA  
 Residues: 1-765 <NEF>  
 Cross-references: GB:U66716; NID:91519443; PID:AA007514..1; PID:91519444  
 Submitted to the EMBL Data Library, August 1996  
 Description: Pub1 acts as an E6-AP-like protein ubiquitin ligase in the degradation of cdc25  
 Reference number: S66562; PMID:96205468  
 Accession: T4159  
 Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA  
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 A;Gene: pub1  
 C;Superfamily: Yeast ubiquitin-protein ligase  
 C;Keywords: ligase  
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 F:288-325;Domain: WW repeat homology <WW2>  
 F:345-382;Domain: WW repeat homology <WW3>  
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 Db 1 MSNAQSRR---IRVTVIAAQLYKDVERFPDPAVLTVDGEQTHTTAIAKTLNPY 55  
 Qy 61 WNCHYDLYGKSDSVTISWNNRKTKHKGAGFCGVRLSNAINRLKDTGYQRL--DLC 118  
 Db 56 WNEFEVNTVDNSTIAIVDQXKF-KKKGGQQLFLGVINLRYGDVLDLAIGDEMILTRDLK 114  
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 185 WERTP-----RPAEYSSSPRPLSCFVDETDPIGTGNGATCGOSDPRAERVSQRH 238  
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 385 -----NVPOQTKRDPLPRKLIFY---LSQPALHPLPGOCHIKYVRNHFED 425  
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49744	robable ubiquitin-protein ligase [imported] - Neurospora crassa	Db	622 EFGVITEEDLIPNGRNIAATNNKKYELMTKRIEGOFRAKDGFFHLIPQDL 631
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	;Species: Neurospora crassa	Db	682 INVDFELELLIGGIAEDVDKXKHTDGYTESDEVIQFWQTFRSDGQKSRLQQ 741
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	;Accession: T49744	Db	742 FTGSRIPYNGKDLQSGPRFTIEKAGEIT-NLPAKHTCENRLLDLPYXSLMNLQQ 800
	;Schulte, U.; Aitn, V.; Boheisel, J.; Brandt, P.; Fartmann, B.; Hoiland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000	Qy	734 KLTAAFEETCGFAVE 748
	;Reference number: Z25022	Db	801 KLTIAVEETMCGFQEE 815
	;Status: preliminary		
	Molecule type: DNA		
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	Experimental source: BAC clone B24B19; strain OR4A		
	Genetics:		
	Gene: NCSP:B24B19.160		
	Map Position: 6		
	Intron: 1/1; 24/1; 59/2; 110/1; 783/2		
	Superfamily: Yeast ubiquitin-protein ligase; WW repeat homology		
	Intron: 239-276/Domain: WW repeat homology <WW1>		
	334-371/Domain: WW repeat homology <WW2>		
	393-430/Domain: WW repeat homology <WW3>		
	Query Match Score: 1521; DB 2; Length: 815;		
	Best Local Similarity: 38.8%; Pred. No. 5.3e-102;		
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2	9 LPVTAADSLVYKRDVERFPFAVATINGE-QTKTROYSKRTLNPKWNEHDFLWLQRSKV 67		
3	70 GKSRSITSVSNWKKHKKRKGAGFLGCYRL-LSNAINRLKDTGYCRL--DLCKLGPNND 126		
4	68 NEDSILAVQVFDDOKKF-KKKDQGFLGVINVIGDTEIADAEMLTRDLKK--STDNL 124		
5	127 TYRQIQIVVSLO-----SRDRI-----GTG 145		
6	125 VNGKLINLSNLATMSRLGPPSSRSPSLTPPOSVISNDRANERPSSAMGGPNNTA 184		
7	146 GQYVDCSR-----LFDND--LFDG 162		
8	185 NNNTLASPASIAVSSSSTAFTPGTNTGATPINSTLVPAQAHHSHTLSLSPEDSMGLPAG 244		
9	163 WEBRTASGRQIQLNHITRTQWERPTRPASEYSSPGRPLSCFYDENTPI-----212		
10	245 WEREDHILGRTYYDINSRTSWNRT-----GTGAENRNTAFTANTOVERQRHNRNTL 297		
11	213 ---SGTNGATCGSSDPRLLERRSRNSRTHLHTP--PDLPPEGYEORTTOQGO 266		
12	298 PEDRTGAN-----SPTLQQQAATAANATAATMHTGATTPTGTGELPAGWBORFTPGR 349		
13	267 VPFHLTGWSVWHDPFVPRL-----SNIN-----CEEBGLPPLPSWEIRNTAIGRV 313		
14	350 PYFVDNTNRTTWDPRRQQTIRMQGQNNTGTTQQPVWSQEWRLNTPARV 409		
15	314 YFVDHNRTTOFTDPRLSANLHVLNQNQLKDQQQQVVSICBDTCECLTYPRKEDLV 373		
16	410 YFVDHNTKTTWDPLPSSI-----DQ-----NYQYKDR 442		
17	374 QKLKLRQELSQOOPQAGHCRIEVSREEIPEESTQVMKMRPKDVLWKLMIKFRGEGLD 433		
18	443 RKLRYFPSQ-PAMRIMSGOCHIKVRSHIFEDSPALEISQSADLKLGRMLINFGEDGLD 501		
19	434 YSGVARWLYLISHMLNPYGLFQYSRDIYQIINPSAVNPEHLYFHVGRTMGMA 493		
20	502 YGGLSRREFFLSENPPFCYLSYSAHDNYTQINPSGIPHEHNFKEFIGVYGLA 561		
21	494 VPHGHYIDGFTLPFKQLGKSITLDDMEVLVDFDLRSLWVLENDITGVLDHTPCVEH 553		
22	562 IFRHRDIAFIGALYKOMLGKAVLADMEGVDIDFHSLSQWMDND-TDVDASTEST 621		
23	554 NAYGETIQHELKPNGRGSIPVNEENKEYVRLYTNWRFGLGIEAQFLAQKGFMENYIPQHL 613		
	Db	119 KLGENDNTDVTGCGT-----SIQSRDRIIGTGTGQVWVCSR--- 153	
	Qy	120 K-SNDGMAVSGRLIVVLSKUPSSSPHSQAPSGHTASSINTSSTRNGHSTSSTRNHS 177	

154	- - - - -	LFDND - - - LFDGWEV	165
178	TSHPSRGITQAVESTLQSGTTAAATNTTSHRSNTSSATRQSSPEFQYGRLLPPGWER	237	
166	RRTASGRIQYLNHTRTTOMERPRPASE	210	YSSPRPISCFVDENT
238	RTDNFGRTYVVDNTTRTTWKRIPTDQTAERGNQLNANTELERHQHCRTRPGCGSSSDS	297	-----
211	- - - - - PISG - - - TINGATCGSSDPRILAERRVRSQRHRNTMRSRTHLT	249	-----
298	SVTYQVGGSNNIPPNQAAAAAFAATGGT-TSGLG- - - - -	331	-----
250	PPDDEPEGYEORTTIOQGVYFLHTQGVSPTWHDPVRDLSNIN-----	299	CEEGLPL
332	- - ELPGNGWORFTPEGRAFVHDNTTRTTWDPRQOYRTYGTNTTQQQPVSQLGPL	389	-----
300	PPGBEIRNTATGRTYFVDENNRNTQFDTBRLSANLHLVLRNQNQLODQQQQVYSLCPDD	359	-----
390	PSGHMERMINTARYFDINTKTITWDPLRPLL-----	426	DQ
360	TECHTPRYKRDLYQKLKLRLQELSQQOOFQ-----	415	AGCHRIEVSSREEETPESEYRQVMXMRP
427	- - - NVPQIKRDFRKIVYFR-----	477	SQPALRILPGQCHIKVRKRKNIFEDAYOBIMRQTP
416	KDIAWKLRLMKFRGEGLDGGVAREWYLISHEMLNPYGLQYSRBDIYTQINPNSAV	475	-----
478	EDLKAKRLMKKFDPGEGLDGGVSE-----	537	FPLFEYSAVNYTONQINPNSGI
476	NPEHLSYFHFVGRIMGMAVPHGHYIDGGFTLPFKQOLLGKSITLDMDMLVDPDLHNSLW	535	-----
538	NPEHLNYYFKPIGRVYGLGVYFHRRLEDAFTVGALYKMMRLRKCKVVLQDMGVDAEVYNSLNW	597	-----
536	LIENDITGVLDTHTFCVEMHAYGETIQLHELKPKNGKSIPYNBENKEVYVLYANWRFLRQCIE	595	-----
598	MLENISDGVDLTLTISADDERFGEVYTVDLKPDGRNIEVTDGNNKEYVELYTORIVDRVQ	657	-----
596	AQFLALQKENGNEVTPQHLLKTFDKELELJTGKIDYNDWKVNTLKJCTDSNTVYK	655	-----
656	FWKAVEFFDEERRARLQLQFTVGSSRPVLOGFKALQAGAPRFLTIHQIDACTNLPKAHT	715	-----
716	CENRIDIPYESYEKLKEVLITLAETTCGFAVE	748	-----
777	CENRVDLPOVYDMSMKQLTLAVETTICFGQE	809	VQOLPKSHT
585	quitin protein ligase - fission yeast ( <i>Schizosaccharomyces pombe</i> )		
586	species: <i>Schizosaccharomyces pombe</i>		
587	date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2000		
588	accession: T39585		
589	submitted to the EMBL Data Library, August 1997		
590	reference number: 221865		
591	accession: T39585		
592	preliminary; translated from GB/EMBL/DDBJ		
593	molecule type: DNA		
594	5'-----		
595	-----3'		

**MULT 5**  
 T39585 Quinolin protein ligase - fission yeast (Schizosaccharomyces pombe)  
 Species: Schizosaccharomyces pombe  
 Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 18-Aug-2000  
 Accession: T39585  
 Holckert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
 Submitted to the EMBL Data Library, August 1997  
 Reference number: Z21865  
 Accession: T39585  
 Status: preliminary; translated from GB/EMBL/DDJB  
 Molecule type: DNA  
 Residues: 1-786 [VOL]  
 Cross-references: EML:Z99759; PIDN:CA016903.1; GSPDB:GN00067; SPDBC16E9.11c  
 Experimental source: strain 972h-; cosmid c16E9  
 Genetics:  
 Gene: SPDBC16E9.11c  
 Map position: 2  
 ntres: 60/2  
 superfamily: yeast ubiquitin-protein ligase; WW repeat homology  
 <WWR>  
 <WWR2>  
 <WWR3>  
 <WWR4>

RESULT 6  
 T46412  
 Tetratricopeptide repeat domain containing 1B  
 NEDD4 - human (fragment)  
 DRKZpp34P2422.1  
 hypothetical protein DRKZpp34P2422.1  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 03-Jun-2002  
 C:Accession: T46412

:Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
Submitted to the Protein Sequence Database, January 2000  
Reference number: 223034  
Accession: T46412  
Status: preliminary  
Molecule type: tRNA  
Residues: 1-820 <AAA>  
Cross-references: EMBL:AU137469  
Experimental source: adult testis; clone DKFZp434P2422  
:Genetics:  
:Gen: GDB:NEDD4  
:Note: DKFZp434P2422.1  
:Keywords: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiquitin ligase Nedd4 - rat (fragment)  
:Superfamily: ligase  
:KeyWords: ligase  
:142-179/Domain: WW repeat homology <WWR2>  
:342-379/Domain: WW repeat homology <WWR3>  
:393-410/Domain: WW repeat homology <WWR3>  
:489-884/Domain: ubiquitin-protein ligase homology <UBI>  
Query Match 33.8%; Score 1364.5%; DB 2; Length 820;  
Best Local Similarity 37.1%; Pred. No. 1.2e+90;  
Matches 315; Conservative 115; Mismatches 221; Gaps 25;  
/ 50 TDYKNTLDPKINQHYDLYIGKSD-SVTISVWNHIIKHKQGAGLGCVR----- 98  
2 69 PTMVERPYTFKDFPLPRSHKSERKGPFPLRKYAMPNG---GDEENSDQRDDMEHW 123  
/ 147 QVVDTCRSRLFDND-----LPDGMEERRTASGRIQYLNHHTRTQWERPT---- 189  
2 124 EVND---SNDSASQHQEEELPPPLDPGLP-----PLGQYDVPVLSPHLPTED 68  
/ 99 -----LLSNAINRLDKTDYGRDLCKLQNDNDTVRGQIVVLSQRIGCG 146  
2 179 SSESDDNNTRQINQEAIRRFRRSRHHSDELPEPSEGDPYEPET-ISEEVNTAGDELG 237  
/ 217 -----GATCQGSSDPR-LAF--RVR-----SORHNNTMSTHL----- 247  
2 238 LALPPPASPGRSRTSPQELSEELSRRLQITPDNSNGEOFSSLQIOPBPSSLRCSVTDAVA 297  
/ 248 --HTPPD-----  
/ 190 -----RPAEYSSP-----GRPLSCFYDENTPISGTN----- 216  
2 191 -----RPAEYSSP-----GRPLSCFYDENTPISGTN----- 216  
/ 218 -----RPAEYSSP-----GRPLSCFYDENTPISGTN----- 216  
2 298 EGQLHPPGAKDPSVYRRAVKDTLSNPQSPQSPYNSPKQHVTKTQSFLPGWERIAANGR 357  
/ 267 VIFFLHTQTGVSTWHDPPVP----DRDLSNINCEEEG2LPPGWETRNTATGRRVYFVDHNNR 321  
2 358 PFTIDHNTKTITWEDPFLKEPFYHMRSKTSINPNDGFLPPGWERIHDGTRFVHDNSK 417  
/ 322 TTOFTDPLRSANLHLVNLNRQNOKQQQQQVSLCPDDTECLTYPR--YKRDLVQTKIL 379  
2 418 TWDPPFL-----QN-----  
/ 380 RQEISQQPQAGHRCTIEVSREEIFFERSYQWMKPDKLNK-RLMKIKERGEGLDYGGVA 438  
2 450 RKCLKKPADIPRFEMKLHRNTFEESYRTMSYRPDKPEKARLQVYDGFY 449  
/ 439 REWYLISHEMNPYGYLFOYSRDIYTQIQINPDSAV-NPEHISYHFYGRIMGAYFHG 497  
2 510 REWEFLISKEMNPYGYLFEESATONYTQINPENGCLNEDHLSYFTFGRYAGLAFFHG 569  
/ 498 HYTDGGFLPLPKYQLGKSIUDDNELVPPDLANSWLLENDITGVLDHHTFCVEHAYG 557  
2 570 KULDGFTRPFYKMLGKQTLINDMSEYYNSLXWLENDPT-ELDLMFCIDEENFG 628  
/ 558 ETIQHELKPNGSISIPNEENKEYRLYNNWRFLRIGIEAQFLAQLQGFNEVIFQHLLKTF 617  
2 629 QTYQDLPKNGSEIMWNTNENKREYDVLVQFRUNTVQKMNIALEGETTELLIDLIKIF 688  
/ 618 DEEDELLIICGKIDYNDWKFNTIRLK--HCTPDSNIVWFKAVEFFDEERRARIQFV 675  
Db 689 DENELELLMCGUGDVFVNDWKRQHSITYKNGYC-PNHPIQFWKAVLMDAEKIRLQLQFV 747  
Qy 676 TGSRYVPLQGKALQGAAGRLFTHQIDACTNLPRKHTCFPRIDPYPYEYKLYEKL 735  
Db 748 TGTCSRPMNGPAELYGSNGFQLFTIEQWGS-PPEKLPRAHTCFNRLDLPYETFEDLREKL 806  
Qy 736 LTAAIEFTCGF 745  
Db 807 LMAVENAQGF 816

RESULT 7  
S70642  
ubiquitin ligase Nedd4 - rat (fragment)  
C.Species: *Rattus norvegicus* (Norway rat)  
C.Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 18-Aug-2000  
R:Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.  
EMBO J. 15, 2371-2380, 1996  
A:Title: WW domains of Nedd4 bind to the proline-rich PY motifs in the epithelial Na+  
A:Reference number: S70642; PMID:96221297; PMID:8665844  
A:Accession: S70642  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-887 <STA>  
A:Cross-references: EMBL:U50842; NID:91293646; PID:AA84949.1; PID:g1293647  
C:Genetics:  
A:Gen: Nedd4  
C:Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiquitin ligase  
C:Repeat: WW repeat homology <WW2>  
F:246-283/Domain: Protein kinase C C2 region homology <WW2>  
F:402-439/Domain: WW repeat homology <WW1>  
F:459-496/Domain: WW repeat homology <WW3>  
F:555-881/Domain: ubiquitin-protein ligase homology <UBI>  
Query Match 33.6%; Score 1355.5%; DB 2; Length 887;  
Best Local Similarity 37.1%; Prod. No. 6e-90;  
Matches 314; Conservative 131; Mismatches 248; Indels 153; Gaps 25;  
/ 14 LRLTIVLACKNLYKCDFFRLPDPKAVV---YTGSCGCHSHSTDVNTLDPKWNOHYDLY- 68  
2 77 VRVKVIAGGLAKKDILGASDPTVTRVLYDPMNSGVLTSQIKTKLGSLNPKWNEET-LFPR 135  
Qy 69 -IGKSDSTVTSVNNHHKKLHKKQGAGFLGCVR-----LLSNAIN 105  
Db 136 VLPQQRH1FVEFBNR1TRDD---FLGQVDPYLPPTENPRMERPYTFDFVFLPRSH 192  
Qy 106 RLKDTGYQFLDLCKLQGNDNDTTRQIVVLSQSRDRIGTGGQVND---CSRL---FDN 157  
Db 193 KSVRYGYLLKMKYMLPKNGSDD----ENADQAEELEPGKVVNLQDPAATHLCHPPEPS 246  
Qy 158 DPDDWEEERTASRQIQLNHTRTTOWERPT-----RPAS 193  
Db 247 PLPPPEWEERQDVGLRTYYVNHEERTTQWKRPSPEDDLDDENGDIOLQAHGAPTTTROIS 306  
Qy 194 E-----YSSPGRPLSCFVDETPISGTTNGATGQSSDP---RRAE----- 230  
Db 307 EDWDGPDNHESPEWNEVYIREDENTIXS-QAQSPPSGHCEPQVLAEDTRLMGNP 365  
Qy 231 ---RVRSSRH--RNYSRT-----HLHTPDLPLPGYEGORTTOQVYFLHTQT 274  
Db 366 ATSQDVTSSNHSSRGSSQTCFEEBQPTLPLPTSSGLPPBGWEBQDDGRSRYVDHNS 425  
Qy 275 GVSTWHDP-----RPP-----RDLSNINCEELGLPPGNEIRATGRYEVDFNNRRT 323  
Db 426 KTIVWSKPTMDODERSKIPAHJRGKTRVDSNDLGPQPGWERTTDGRVFFFINNIKCT 485  
Qy 324 QFTPPRISANLHLVNLNRQNOKQQQQVSLCPDDTECLTYPR--YKRDLVQTKILQEL 383  
Db 486 QWEDEPM-----ONAVITGPASP-----TSRDYKRYEFERRKL 519  
Qy 384 SQQPQAGHCRIVSREEIFERSYQWMKPDKLNK-RLMKIKERGEGLDYGGVA 438

3 520 KKQTDIPKFKMRRANILEDSSYRIMGVKRADFIKARLWIEFFGEKGLDYGGVAREWF 579  
 4 443 YLLSHEMNPYGYLFOYS-RDPIYTLQINPPSAV-NPEHLSYPHFGRIMGMAYFCHYI 500  
 5 580 FLISKEHENPYGYLFOYS-SATDNTYQINPNGLNEDHSYFKEIGRAGMAYHGRLL 639  
 6 501 DGAFTPFLPKQKLGSITLDMDLYLPDLNSLYMLNLENDITGVLDDHTFCVEHNAYGBII 560  
 7 640 DGFPIRTPYKMLQKLTHIDNDSOSEYSSSLRVLLENPT-BDLRLTIDBELFGOTH 698  
 8 561 OHELKPGKSTPVEENKEYVRLYTNWREFRGIAQFLAQKGRNEVTPQHLKTFDEK 620  
 9 699 QHELKPGSSEVVTTNKRKEITYLVIQWRPVNRICKOMAKFESFPQDLIKIFEN 758  
 10 621 EFLFLICGLGKIDVNDKONTRLKH-CTPSNIVKFWKAVFDEERBARLQFTGSS 679  
 11 759 EFLLMCGLGDYDVMWRHETKVKYCNCSLNHOVTHFWFCAVLMDSERRIRLQLQFTGTS 818  
 12 680 RVPLQGKALQGAAPLFLTHIQIACTNNLPAKTCPRID-PPYESYEKLYEKLJTA 739  
 13 819 RYPMNGFAELYGSNGSPOSFTVEQW-GTPDKLUPRAHTCFCNLDPYSESDELWDQLOMAI 877  
 14 740 EBTGCF 745  
 15 878 ENTOGF 883

16 SULT 8  
 3196 3196  
 Species: Mus musculus (house mouse)  
 Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 18-Aug-2000  
 Accession: T37000  
 Kumar, S.; Tomooka, Y.; Noda, M.  
 Ochem, Biophys. Res. Commun., 185, 1155-1161, 1992  
 Title: Identification of a set of genes with developmentally down-regulated expression  
 Reference number: 160167; PMID:32328780; PMID:11379265  
 Accession: I83196  
 Status: preliminary; translated from GB/EMBL/DBJ  
 Molecule type: mRNA  
 Residues: 1-708 <RES>  
 Cross-references: GB:D10714; NID:9220508; PID:9220509  
 Genetics:  
 Gene: NEDD-4  
 Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui  
 40-77/Domain: WW repeat homology <WW1>  
 195-233/Domain: WW repeat homology <WW2>  
 251-288/Domain: WW repeat homology <WW3>  
 347-682/Domain: ubiquitin-protein ligase homology <UBI>

Query Match  
 Best Local Similarity 29.1%; Score 1177; DB 2; Length 708;  
 Matches 260; Conservative 40.4%; Pred. No. 3.7e-77; Gaps 17;

159 LPGNBERRTASGRIOYLNHTRTRTQWERPT-----RPASE 194  
 42 LPGNBERERQDVLGRYYNNRSRTRTQWERPSPPDDLTDEDNDMQLQAQRAFTTRQISE 101  
 195 -----YSGDGRPSCSFCFDENPIG-----TNGATCQQ--S 223  
 102 DVGDGPDRNPREPENTLIVREDENTEYSGAQVSPSGHIDVQTHLAEEFNTLAVCNPAT 161  
 224 SDPRAEERRVSQRHNRMSRTH-----LHTPPDLPPEGYEORTTQOCQSYFL 270  
 162 SQP-----VTSNSHSSRCGSLQTICIFEQPFLPVLPPTSSLPPWEERDDRSRYY 215  
 271 HTQTVSTWHDPLP-----RVPEDL-S-NINCBELGIPPPGWEIRNTATGRVYFYDHNNR 321  
 216 DHNSKTTTWSKPTMDPDRSKPAPHLRKTDNSLGLPUPGMBERTHDTGRVFFINHNIK 275  
 322 TTOEDPRLSANLJUWLNQNQLKDQQQVUSLCPDDTECLTVPRKRLVQKUILLRQ 381  
 276 KTQWDPRL-----ONVATGIP-----AvP-YSDYKRYTEFFRR 309

Qy 382 ELSQQPOA GHCRILEVSREEIPFESYQVMQRPKDQWIK-RIMMIKPRGEGLDYGCGVARE 440  
 Db 310 KLRKTDIPKFKMRRANILEDSSYFGRIMGMAYFCHYI 369  
 Qy 441 WYLISHEMLNPYGYLFOYSRDIYTOINPSAV-NPEHLSYPHFGRIMGMAYFCHYI 499  
 Db 370 WFLLSKENFNPYGYLFOYSATDNTYQINPNGLCNEHDHSYFKEIGRAGMAYHGRKL 429  
 Qy 500 IDGGTLPYKQOLGKSTLDMDLYLPDLNSLYMLNLENDITGVLDDHTFCVEHNAYGEI 559  
 Db 430 LDGFPIRTPYKMLQKLTHIDNDSOSEYSSSLRVLLENPT-BDLRLTIDBELFGOT 488  
 Qy 560 IQHJLKPNGRSIVPNENEKKETVRLYNNWRFRLGJBAQFLAQKGFNEVIFQHJLKTDFE 619  
 Db 469 HQHLKTGSEETIVTWNKKEVYLYLQWRFYNROKQMAAFEGFPFLPDLLKIFDE 548  
 Qy 620 KEFLLIICGLGKIDVNDKVNTRLKH-CTPDSNIVKFWKAVFDEERARLQFVTGTS 678  
 Db 549 NEFLBLLMCGLGDVNDWREHTKVKYNSMNHQIHWFWKAVMMNDSEKIRLQLQFVTGT 608  
 Qy 679 SRVPLQGKALQGAAGPRLFTHQ---IDACTNNLPK-AHTC 716  
 Db 609 SRVPMNGFAELYGSNGSPOSFTVEQW-GTPDKLUPRAHTCFCNLDPYSESDELWDQLOMAI 651

RESULT 9  
 T37000  
 probable ubiquitin-protein ligase - fission yeast (Schizosaccharomyces pombe)  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 03-Dec-1999 #Sequence\_revision 03-Dec-1999 #text\_change 18-Aug-2000  
 C;Accession: T37000  
 R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, September 1999  
 A;Reference number: 221752  
 A;Accession: T37000  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-671 <RTE>  
 A;Cross-References: EMBL:AU11390; PID: CAB55856-1; GSPDB: GN00066; SPDB: SPAC1-805-15C  
 A;Experimental source: strain 972h; cosmid c1805  
 C;Genetics:  
 A;Gene: SPDB:SPAC1805-15C  
 A;Map position: 1  
 A;Introns: 60/2; 105/1; 639/2  
 C;Supergfamily: WW repeat homology <WW>  
 F;242-279/Domain: WW repeat homology <WW>  
 Query Match  
 Best Local Similarity 25.9%; Score 1046.5; DB 2; Length 671;  
 Matches 257; Conservative 33.9%; Pred. No. 1e-67; Mismatches 263; Indels 113; Gaps 17;

Qy 13 KLRITLVCAKLVKKDFRFLDPFAKVNIDPGQCHSPTDVTWNLDPKWNQHYDLYIGKS 72  
 Db 7 EVQLTILHVGEIWNKNGLRLSRISKPVLLISVD-DDQFIKTNVAVSGTLRLSWGFTQKLTVSPQ 65  
 Qy 73 DSVTISWNHKKIKKQGAFLGCVYRLSNA---INRLDTGYDLCKLGPNDNDTFR 129  
 Db 66 SILLQFLDEQ-KNETSDPSDFVGLGAAVVNSPLFNNPKDDYKTRITL---RSPGSSYR 120  
 Qy 130 GQIVVLSQSRDRIGTGQVYD---CSRLFNDLDPDGWEERRPASGRIOYLNHITRCTQW 185  
 Db 121 GS-VVCLPFRSKPLPBLPADKSQICTDIDASGCAMTRIDEFGHVVYL-----170  
 Qy 186 ERPTPASEYSSPGRPLSCFVDETPISGNTGQGSSDPRLAERRYRSQRHNRMSR 245  
 Db 171 -----KSP-----QSVISATISHELENLTPKQ-----VFSQFLFNNGSKS 209  
 Qy 246 HLHTPPD-----LPGEGYQRTTQGQVYFLHTQGTVSTWHDPRVPRDLSNINCBEIGPL 299  
 Db 210 SIRNLNYKVHLJLIEHYHALSTRQQV-----AVERGPL 244  
 Qy 300 PPGWEIRNTATGRVYFVDHNINRTQFTDFR-----LSANLHLVLRNQNOLKDQQQQ 351

245	PAGWNRLLSDYHYYFDVISTKTTWSDRDNVASYSENTDSI---QQINDEYQRK 300	Db	3096 NQEQLLELLISGLPEDIIDWKWAKNTTEYHGYNVSSPQVQMFWRAVRSFDEERAKLQLPATG 3155
352	VVSLLCPDDTECLTPRYKEDLVQKLRQELSQOPQAGHRCEVSREEEFEESYRQVM 411	Qy	678 SRYVPLOGPKALOGAAGPPLFTIHQIDACTNNLPKAHTCFCNRIDIPPYESYKLYEKLTF 737
301	IA-----YMD-----REPMANNDQ--LQKVRBATTEDDIIS 335	Db	3156 TSKVPLNGKXELGENMSGFRNTHKSYSLSNRPQSHFCNFQDLPEDTYQRLSMLT 3215
412	KMRKDILWKLRLMIKFERGEELDYGSEARWMLYLISHMNPYGLFOYSRSDRDIYTQIQLQINP 471	Qy	738 AIEETC---GFA 746
336	KLSVSDMKKKLILPRNECDLDYGVSRREFFYLISHA.FNPGYSLFEATDDNYGLQISP 395	Db	3216 AINESEGFGFA 3227
472	DSAYAVERHLSYFHFVGRINGMAFPGHYDGGFLPFYKOLJKGSITLDDMELYDPHLN 531	RESULT 11	
396	LSSVNPDPSFYFRFGRYGLAITHRYLDVQTVLPFKTRILQRPCLIEDYRDVDEVYYE 455	T49719	related to TOM1 protein [Imported] - Neurospora crassa
532	SLVNLENDDTGVLQDHHTFCYHEVNAHYGEILOHQELPKNGKSIPIUNENKEYVBLVYNNRFL 591	N	Alternate names: protein B11B22.10
456	SLKWKRNNDKEDESLQLNFSVTEENFGSESTVDLIPNGNATVNNQNKYHALTBHKLV 515	C;Species:	Neurospora crassa
592	RGIBAQFLAQKGNEVIPQHLLKTFDEKELELLIGLGKIDVNDWKNTTRLKHCTPDSN 651	C;Date:	02-Jun-2000 #text_change 02-Jun-2000 #text_change 02-Jun-2000
516	TSTFQFNALKGGINELPDSVQIFENENELDTLNGRDRDIDVQDWKRFTDYRSTYETDD 575	C;Accession:	T49799
652	IYRFWKAVERFPDERRABLQFTVTGSSRVPLQFGKALQGAAPRLFTIHQIDACTNNLP 711	A;Reference number:	225022
576	IVTNEWELSESSPEKKAKLQFPTGTSRLPLSGFDMEHGSDGPRKFTIERY-GHISQLP 634	A;Accession:	T49799
712	KAHTCENRNDIPIPESYERLYEKLLTAIEETCGFAVE 748	A;Molecule type:	preliminary
635	KAHTCENRNDIPIPNSKEEQLKLTIAQETAGFTE 671	A;Residues:	1-3839 <SCHE>
		A;Cross-references:	ENBL:AU356834; GSPDB:GN00116; NCSP:B11B22.10
		A;Experimental source:	BAC clone B11B22; Strain OR74A
		C;Genetics:	
		A;Map Position:	NCSP:B11B22.10
		A;Introns:	16/3; 2607/1; 2623/1; 2658/1; 2845/1; 2987/2; 3204/3; 3694/1; 3809/1
		Query Match	21.0% Score 846.5; DB 2; Length 3839;
		Best Local Similarity	21.0% Score 846.5; DB 2; Length 3839;
		Matches	168; Conservative 79; Mismatches 128; Indels 17; Gaps 4;
		372	LYOKLKIL-----RCQELSOOPOQAGH----CRIEVSEBEFEESYQVMKRPKDL 418
		3448	LVNPKVQSFDFNCRNYYFNRSVKSYQOTRHSFPPLQVQRVERHFDSFRSLYYKKADEL 3507
		419	-WKRBLMIKFRGEGLQDGGVAREWLWYLISHEMLNPYGLFYSRSDIYTQINPDSAVNP 477
		3505	KFGKLNTTRFGQEGVGDAGGVTRNEWFQVLSRQMDPDKVYVLFPLQVNLSPIND 3567
		Db	QY 478 SHISYFHFVGRIMGMAYFHGHVTDGSPFLPKQLGKSITLDDMELVDPDHLNSLWIL 537
		Db	35568 EHUPPFKIGRILKALYEGRILECYPSRATYKRLGKPVSKOMESFDDYKSLVWML 3627
		Qy	538 ENDITGVDHTPCVNEHAYGETIQLHLKPNSKISIPNNEENKEYRTLYNWRFLRGIEAQ 597
		Db	3628 ENDITDILITETSVEDDVFGEVKTDIENGNIPITEEENKEYTFLVHLKLTISVQDQ 3687
		Db	598 FLALQRGFNEVIPQHLLKTFDEKELELLIGLGKIDVNDWKNTTRLKHCTPDSNIVKWPW 657
		Db	3668 MAFLTGHIELIPEELIAFQELLELLSSLPDIDDKRANTHYNYSAGAPIQFWF 3747
		Db	3798 KAYEFFDEERPARLILQFVTGSSRVPLQGKALQAGAIPRFTIHOIDACTNNLPKAHTCF 717
		Db	3748 RAVRSFDEKEELRKLQFVTGTSKVPLNGKFELEKGNGVSRFNTHRDYGSKDRLPSHTCF 3807
		Qy	718 NRDIPPEYESYKLYKQFLPAI---BETCGFA 746
		Db	3808 NQDLPPEYENTLRSOLLXAITAGSSDDYFSPA 3839
		RESULT 12	
		T01491	ubiquitin-protein ligase homolog F1707.15 - Arabidopsis thaliana
		C;Species:	Arabidopsis thaliana (mouse-ear cress)
		C;Accession:	T01491
		R;Yvonne Saito, V. S.; Schwart, C.J.; Shinn, P.; Sun, R.W.; Davis, R.W.; Federer, T.P.; Federer, I.	
		rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, R.W.; Davis, R.W.; Federer, T.P.; Federer, I.	
		558	EIQHEIKPNSGSIPIUNENKEYVLYNNWRFRLERIEAQLFLAQKGENEVIPOHLLTF 617
		3036	EKTVDLIPGRNPNYPTTELKNVYNTMVDKLRLRSVQDQLKSLIDGFDTIPLSHLQIF 3095
		618	DEKELELLIGLGKIDVNDWKNTTRLKHCTPDSNIVKWPWKAEEFDEERPARLQFQTG 677
		2976	TRELQVLAQRNMPDZALEFLPVGTGATTEFPRNRSVSNPHLSLSPKFFIGRIIGKALYDG 2975
		498	HYDGGFTPLPFYKQJLGKSIITDMDMELVDPDHLNSLWILENDITGVLDHTFCYEHNAYG 557
		2958	EIQHEIKPNSGSIPIUNENKEYVLYNNWRFRLERIEAQLFLAQKGENEVIPOHLLTF 617
		3036	EKTVDLIPGRNPNYPTTELKNVYNTMVDKLRLRSVQDQLKSLIDGFDTIPLSHLQIF 3095

submitted to the EMBL Data Library, June 1998  
 Description: Arabidopsis thaliana chromosome 1 BAC F1707 sequence.  
 Reference number: Z14334

Status: translated from GB/EMBL/DDBJ

Molecule type: DNA

Cross-references: EMBL:AC003671; NID:92833627; PID:93176690; GSPDB:GN00059; ATSP:F1707

Experimental source: cultivar Columbia  
 Genetics:

Gene: ATSP:F1707.15

Map position: 1

Introns: 118/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2

Superfamily: ubiquitin-protein ligase homology <UBI>  
 756-1120/Domain: ubiquitin-protein ligase homology <UBI>

Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

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Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

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Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

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Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

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Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

Query Match Score: 805.5; DB: 2; Length: 1126;

Best Local Similarity: 41.3%; Pred. No. 6.5e-50;

Matches: 177; Conservative: 63; Mismatches: 142; Indels: 47; Gaps: 7;

A;Residues: 1-4056 <STO>  
 A;Cross-references: GB:AE005173; NID:g8778329; PIDN:AAF79338.1; GSPDB:GN00141

C;Genetics:  
 A;Gene: F14J16.10  
 A;Map position: 1

Query Match Score: 19.9%; Best Local Similarity: 40.0%; Matches: 177; Conservative: 62; Mismatches: 143; Indels: 60; Gaps: 7;

Qy 363 LTVYKRDVLQKLKIRQELSQQQPQ-AGHRICREVSREBEEFSYQVMKOREPKDLWK 420

Db 3617 LKAPRL-IDFDNKAYRSRTRHQDHISPLRQVLLKTFQDPLNSLYWILEND 540

Qy 421 RLMKFERGEGLDGGYVAREMYLJSHEMLNPYGLFQSRSRDLITYLQINPSAVNPEH 480

Db 3795 VSDIDLQFSMDAEEKHILYKTEVRLMCFCLPFWCFCIPKCHCIELITLSMKKVDY 3854

Qy 759 RANVQFQGEEGIDAGGTREYVQLSRVIFDKGALLFTVGNDA-TFQPNNPSVYQTBEHL 817

Db 3855 ELLKGKSKIPDNEBNKEYVRLVNVRFRLRJEQAFLQXGFNEVIPHLLKFDFEKL 622

Qy 481 SYFHFGVRIMNAVIGHYLDGGFLPFPYKQLLGSLTDDMELVDPLHNSLWILEND 540

Db 3856 ELLIGLGLKID--VNDWKVNTTRKHCPTDPNSVWFKAVEFDEER 667

Qy 818 SYFKFGVRMVKALFGQQLDVYFRSPSYKHLGVKTYHDIAVDPPYKQNWKILEND 877

Db 3915 ELLISGLPBIDCKLDS-IDQYLCAPILDLKANTEXTSYTAGSPVHWKEVVAFKSKED 3974

Qy 878 VSDIDLQFSMDAEEKHILYKTEVRLMCFCLPFWCFCIPKCHCIELITLSMKKVDY 937

Db 3975 MARFLQVTGTSVPLEGKALQGIISSPQRQLQHKGADPERLPSAHTCFNQLDPEYQS 4034

Qy 728 YEKLKEULTAETETC--GFA 746

Db 4035 KEQLQERULLATAHESEGFQFA 4056

RESULT 14  
 S6925 RARUQFYTGSVSVPLQGFKALQGAAGPRLFTQHIDCTNPLKAHTCFNQLDPEYQS 727  
 hypothetical protein YDR457w - Yeast (Saccharomyces cerevisiae)  
 C;Species: Saccharomyces cerevisiae  
 C;Date: 22-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 23-Mar-2001  
 C;Accession: S6925  
 R;Dietrich, P.S.  
 submitted to the EMBL Data Library, August 1995  
 A;Description: The sequence of *S. cerevisiae* cosmid 9410, 8035, 8166, and 9787.  
 A;Reference number: S69554  
 A;Accession: S69615  
 A;Molecule type: DNA  
 A;Residues: 1-3268 <DTB>  
 A;Cross-references: SGD:S0002865; MIPS:YDR457w  
 A;Map position: 4R  
 Query Match Score: 19.5%; Best Local Similarity: 45.7%; Matches: 164; Conservative: 59; Mismatches: 132; Indels: 4; Gaps: 2;

Qy 384 SQQOPQAGHCRIEVSREBEEFSYQVMKOREPKDLWKLMIKRGEEGDLGYGGVAREWL 442  
 Db 2905 NQERPK--LPITVNRQVFLDSYRALFFTNDEIKNSKLEITKGESSVDAVVTVREWY 2961

Qy 443 YLISHENMNPYGLFOVSRDIIYTLQINPSAVNPEHLYFHFGRINGMAYGHYIDG 502

Db 2962 QVLSRQHENPDYALFLPVPSDKTTFHPNRTSGINPEHLSFPKIGMIAKIRDQCFLDC 3021



GenCore version 5.1.6  
 Copyright (C) 1993 - 2004 Compugen Ltd.

1 protein - protein search, using SW model

in on: February 20, 2004, 15:25:26 (without alignments)

file: US-10-009-945-4  
 :refect score: 4038  
 sequence: 1 MSENPGRRNGPVKLRLTVLC.....EKLYEKKLTAIEETCGFAVE 748  
 :oring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

:arched: 830525 seqs, 258052604 residues

:tal number of hits satisfying chosen parameter: 830525

:num DB seq length: 0

:ximum DB seq length: 2000000000

:st-processing: Minimum Match 100%

Maximum Match 100%

Listing First 45 summaries

:tatabase : SPTREMBL\_23:  
 1: sp\_archea:  
 2: sp\_bacteria:  
 3: sp\_fungi:  
 4: sp\_humn:  
 5: sp\_invertebrate:  
 6: sp\_mammal:  
 7: sp\_mhc:  
 8: sp\_organelle:  
 9: sp\_phage:  
 10: sp\_plant:  
 11: sp\_rrodent:  
 12: sp\_virus:  
 13: sp\_vertebrate:  
 14: sp\_unclassified:  
 15: sp\_virus:  
 16: sp\_bacteriopl:

17: sp\_archeap:  
 18: sp\_archeap:  
 19: sp\_bacteria:  
 20: sp\_fungi:  
 21: sp\_humn:  
 22: sp\_invertebrate:  
 23: sp\_mammal:  
 24: sp\_mhc:  
 25: sp\_organelle:  
 26: sp\_phage:  
 27: sp\_plant:  
 28: sp\_rrodent:  
 29: sp\_virus:  
 30: sp\_vertebrate:  
 31: sp\_unclassified:  
 32: sp\_virus:  
 33: sp\_bacteriopl:

34: sp\_archeap:  
 35: sp\_archeap:  
 36: sp\_bacteria:  
 37: sp\_fungi:  
 38: sp\_humn:  
 39: sp\_invertebrate:  
 40: sp\_mammal:  
 41: sp\_mhc:  
 42: sp\_organelle:  
 43: sp\_phage:  
 44: sp\_plant:  
 45: sp\_rrodent:  
 46: sp\_virus:  
 47: sp\_vertebrate:  
 48: sp\_unclassified:  
 49: sp\_virus:  
 50: sp\_bacteriopl:

51: sp\_archeap:  
 52: sp\_bacteria:  
 53: sp\_fungi:  
 54: sp\_humn:  
 55: sp\_invertebrate:  
 56: sp\_mammal:  
 57: sp\_mhc:  
 58: sp\_organelle:  
 59: sp\_phage:  
 60: sp\_plant:  
 61: sp\_rrodent:  
 62: sp\_virus:  
 63: sp\_vertebrate:  
 64: sp\_unclassified:  
 65: sp\_virus:  
 66: sp\_bacteriopl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

result No.	Score	Query	Match	Length	DB	ID	Description
1	3041	75.3	728	11	Q8K300		Q8k300 mus musculu
2	2313	57.3	1061	5	Q9V853		Q9v853 drosoephila
3	1910	47.3	376	13	Q9BTS4		Q9bts4 xenopus lae
4	1668.5	41.3	355	11	Q8BSG0		Q8bsg0 mus musculu
5	1552	38.4	288	4	Q96DE7		Q96de7 homo sapien
6	1418	35.1	786	3	Q14326		Q14326 chitikobacch
7	1398	34.6	911	4	Q8NSA7		Q8nsa7 homo sapien
8	1386	34.3	955	4	Q96PU5		Q96pu5 homo sapien
9	1379	34.2	295	4	Q8NDD8		Q8ndd8 homo sapien
10	1378	34.1	258	11	Q9CS23		Q9cs23 homu sapien
11	1364.5	33.8	820	4	Q9NT88		Q9nt88 homu sapien
12	1358	33.6	887	11	Q8BG33		Q8bg33 mus musculu
13	1357.5	33.6	855	11	Q8CP10		Q8cp10 mus musculu
14	1355.5	33.6	887	11	Q9H2W4		Q9h2w4 rattus norvegicus
15	1354	33.5	854	4	Q9H2W4		Q9h2w4 homo sapien
16	1354	33.5	835	11	QBBRR9		Q8brt9 mus musculu

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### ALIGNMENTS

RESULT 1	Q8K300	PRELIMINARY;	PRT;	PRT;	AA.
ID	Q8K300				
AC	Q8K300				
DT	01-OCT-2002 (TREMBLrel. 22, Created)				
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DR	Q9bbk4 caenorhabdi				
DR	Q95tq0 drosophila				
DR	Q8tqc8 drosophila				
DR	Q95xu3 caenorhabdi				
DR	Q9bz23 mus musculu				
DR	Q9n227 caenorhabdi				
DR	Q9bbk4 caenorhabdi				
DR	Q95tq0 drosophila				
DR	Q8tqc8 drosophila				
DR	Q95xu3 caenorhabdi				
DR	Q9bz23 mus musculu				
DR	Q9n227 caenorhabdi				
DR	Q9bbk4 caenorhabdi				
DR	Q95tq0 drosophila				
DR	Q8tqc8 drosophila				
DR	Q95xu3 caenorhabdi				
DR	Q9bz23 mus musculu				
DR	Q9n227 caenorhabdi				
DR	Q9bbk4 caenorhabdi				
DR	Q95tq0 drosophila				
DR	Q8tqc8 drosophila				
DR	Q95xu3 caenorhabdi				
DR	Q9bz23 mus musculu				
DR	Q9n227 caenorhabdi				
DR	Q9bbk4 caenorhabdi				
DR	Q95tq0 drosophila				
DR	Q8tqc8 drosophila				
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DR	Q8tqc8 drosophila				
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DR	Q95tq0 drosophila				
DR	Q8tqc8 drosophila				
DR	Q95xu3 caenorhabdi				
DR	Q9bz23 mus musculu				
DR	Q9				

1 MSNPGRRRNG-PVKLRLTIVCAKNNVVKDFERLPPDFAKVVDGSSGCQHSTDIVKNTLDP 59  
 1 MSNPGRRRNGSSKTTIVCAKNNVVKDFERLPPDFAKVVDGSSGCQHSTDIVKNTLDP 60  
 60 KPNQHDTLYIGRSDDTTISWNKHKKHKKGGAGFPGCYRLLSNAIRNLKDGTGQRDLCK 119  
 61 KRSQHDLVNGKTDTSITISWNKHKKHKKGGAGFPGCYRLLSNAIRNLKDGTGQRDLCK 120  
 120 LGPNNDTIVRGIVYLSQSDRIGTGGVYDCSRFEDNLDLPGWEERTASGRQYQINHI 179  
 121 LNPSDDAVRQIVVSLQTRDRIGGGSVDCRGLLEN-----TVY----- 163  
 180 TRTIVQERPTPASESSSPGRPLSCFEDNTPISTGNTGATCG----QSDDPRIAE 230  
 164 -----EPSPGRPLSCFEDNTPISTGNTGATCG----QSDDPRIAE 230  
 231 RVRVSQRHRNTM---SRTIHLTHPPDLPBEGYEQTTOQQQVYLHTQTGVSYWHDRPR 286  
 210 QRLRNBEVRGLPCTQNRPHQSSPELPGYEQTQVQVYVLTQTGVSYWHDRPR 269  
 287 DLSNINCEELGPPLPGWEIANTATGRVYFDHNNRTTODPBLSANJHLVNQNQLKD 346  
 270 DLNSYNCDELGPPLPGWEVSTSGRIVYDHNRTTQFTDR---LHHNMHQOLKE 325  
 347 QQQQ-QVVSLOPDDECLATVPRKDLVOKLKTLRQELSQQOFGAQHCRIEVSREEFEE 405  
 326 PSQPLQPLPSGSVEEBLPAQRYERDVLVOKLKTLRHELSLQQDQAQHCRIEVSREEFEE 385  
 406 SYRQNMKMRPKDLWCRMLIKFRGEGEGLDGGVAREMYLSSHEMLNYYGLFOYSDDIIY 465  
 386 SYRQNMKMRPKDLWCRMLVKFRGLMVFKRGEGEGLDGGVAREWLCLHEMLNYYGLFOYSDDIIY 445  
 466 TLQINPDSATNPHEUFSYHFVGRIGMGMAVFHGHDGFTLPYKQLICKSITIDMELY 525  
 446 TLQINPDSINPDHSYFEHVGRIMGLAVFHGHYINGEFTVBFYKQOLKGPKIQLSSELY 505  
 526 DPDLENSLYMILENDITGYLDHTRCVERHNAYGIIQHLKENGKS PVNEENKKEVRLY 585  
 506 DPEFLRSLYMILENDITPVLDHTEPEVNEAFAQGILQHELKPGNRYPVTEENKEYVRLY 565  
 586 VNWRRLRGTEAQFLAQKFNEITPQHLLKTPEKELELIGLGKDNDWKNTRLKH 645  
 566 VNWRRLRGTEAQFLAQKFNEITPQHLLKPFOKELELIGGLKDNDWKNTRLKH 625  
 646 CTPDNINIVKWFKAFFDBERRARLLOVTTGSSRVPLQGFKAQGAAPRLFTIHQIDA 705  
 626 CVADSINIVKWFKAFFDBERRARLLOVTTGSSRVPLQGFKAQGAAPRLFTIHQIDA 685  
 706 CTNNPLKAHTCFNIDIPPEYESKLYEKLTAIEETCGFAVE 748  
 686 NTDNPLKAHTCFNIDIPPEYESKLYEKLTAIEETCGFAVE 728

SULT 2  
 V833 PRELIMINARY; PRT; 1061 AA.  
 Q9V833; Q9U3W2; PRELIMINARY; PRT; 1061 AA.  
 01-MAY-2000 (PREMIREl. 13, Created)  
 01-MAR-2003 (PREMIREl. 22, Last sequence update)  
 CG4943 protein (23 ubiquitin ligase) (ubiquitin-protein ligase) (Smad-LACK OR SMURF OR SMURF1 OR CG4943-Drosophila melanogaster (Fruit fly).  
 Neoptera; Mecoptera; Archaeopoda; Hexapoda; Insecta; Pterygota; Ephdroioidea; Drosophilidae; Drosophila.  
 [1] NCBI\_TaxID=7227;  
 SEQUENCE FROM N.A.  
 STRAIN=Birzka; MEDLINE=2019606; PubMed=10731132;  
 Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D., FlyBase; Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RN 99V833 PRELIMINARY; PRT; 1061 AA.  
 RA Q9V833; Q9U3W2; PRELIMINARY; PRT; 1061 AA.  
 RA 01-MAY-2000 (PREMIREl. 13, Created)  
 RA 01-MAR-2003 (PREMIREl. 22, Last sequence update)  
 RA CG4943 protein (23 ubiquitin ligase) (ubiquitin-protein ligase) (Smad-LACK OR SMURF OR SMURF1 OR CG4943-Drosophila melanogaster (Fruit fly).  
 Neoptera; Endopterygota; Diptera; Brachycera; Museomorpha; Ephdroioidea; Drosophilidae; Drosophila.  
 [1] NCBI\_TaxID=7227;  
 SEQUENCE FROM N.A.  
 STRAIN=Birzka; MEDLINE=2019606; PubMed=10731132;  
 Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; FlyBase; Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.



SMART; SM00456; WW; 3.	Db	1 VSREEEIFEESYQTMKMRPKDLKKRLLMVKFRGEEGLDYGGVAREWLYLICHEMNPYYGL 60
PROSITE; PS0004; C2_DOMAIN_2; 1.	Qy	457 FQISDDITLQINPDSAVNPEHLSYHFGIMAVFHRYIDGGFTLPFYKOLLGKS 516
PROSITE; PS01159; WW_DOMAIN_1; 1.	Db	51 FQYSTDNTLQINPDSSTINPDHLSYHFGIMAVFHRYIDGGFTLPFYKOLLGKP 120
LIGASE;		
NON_TER 376 376 AA; 42652 MW; CA6AB2B5F4C20E98 CRC64;		
SEQUENCE		
every March 47.3%; Score 1910; DB 13; Length 376;		
est Local Similarity 94.1%; Pred. No. 1.5e-140;		
atches 354; Conservative 10; Mismatches 8; Indels 4; Gaps 3;		
1 MSNPGRRNGPVLRLTVLCKANLKKDPR-LPDPARTVVDSSQCHSTDTYVNTLDP 59	Db	517 ITLDDMELYDPDLHSYLWILENDITGYLDHTFCVHNAYGBIOHELKENGKS.PVNNE 576
1 MSNQSGRSNGPVLRLTVLCKANLKKDPR-LPDPARTVVDSSQCHSTDTYVNTLDP 60	Qy	518 IQLSPLSDEPLHSLWILENDITGYLDHTFCVHNAYGBIOHELKENGNS.PVNNE 576
60 KNQHQHYDLYIGKSDSTIISWNHKKHKKGAGFLGCVRLLSNAIRNLKDGTQRLICK 119	Db	577 NKEEYVRLVNNWFLRGIAOFALQGFNEYIPQHLLKTDEKELEELIICGLGKIDVND 636
61 KNQHQHYDLYIGKSDSTIISWNHKKHKKGAGFLGCVRLLSNAIRNLKDGTQRLICK 120	Qy	578 NKEEYVRLVNNWFLRGIAOFALQGFNEYIPQHLLKTDEKELEELIICGLGKIDVND 636
120 LGPNNDVYRGQIVVSLSQRDRIGTGSQVYDCSRLFNDLPGMEERRTAGRIQYLNHI 179	Db	637 WKVNTPLKHCTPDSNIVNWFNWKAFFDEERARLQFYTGSSSRYPLQGKALQ--GAA 693
121 LGPNNDVYRGQIVVSLSQRDRIGTGSQVYDCSRLFNDLPGMEERRTAGRIQYLNHI 180	Qy	638 WKSNTPLKHCVADSNIVNWFNWKAFFDEERARLQFVTSTRYPLQGKALQGSGTGAA 300
RESULT 5		
Q96DE7 PRELIMINARY; PRT; 288 AA.		
ID Q96DE7 ID Q96DE7 PRELIMINARY; PRT; 288 AA.		
AC Q96DE7 AC Q96DE7 PRELIMINARY; PRT; 288 AA.		
DT 01-DEC-2001 (TREMBLrel. 19; Created)		
DT 01-MAR-2003 (TREMBLrel. 19; Last sequence update)		
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)		
DB Similar to E3 ubiquitin ligase SMURF2 (Fragment).		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_TaxID=9606; RN [1]		
RN SEQUENCE FROM N.A.		
RC TISSUE=Lung;		
RA Strausberg R;		
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		
DR EMBL; BC009527; AAH09571; -.		
DR InterPro; IPR00056; HECT_domain..		
DR PFam; PF00632; HECT; 1.		
DR SMART; SM00119; HECTC; 1.		
DR PROSITE; PS50237; HECT; 1.		
FT NON TBR		
SQ SEQUENCE 288 AA; 33255 MW; FE2B43E300E66537 CRC64;		
Query Match 38.4%; Score 1552; DB 4; Length 288;		
Best Local Similarity 100.0%; Pred. No. 8.e-113; Mismatches 0; Indels 0; Gaps 0;		
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 461 RDDITLQINPDSAVNPEHLSYHFGIMAVFHRYIDGGFTLPFYKOLLGKSITLD 520		
ISCO QBSSCO; PRELIMINARY; PRT; 355 AA.		
QBSSCO; PRELIMINARY; PRT; 355 AA.		
01-MAR-2003 (TREMBLrel. 23; Created)		
01-MAR-2003 (TREMBLrel. 23; Last sequence update)		
Hypotheoretical HECT domain (Fragment).		
Mus musculus (Mouse).		
Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi;		
Murinae; Muridae; Sciurognathi; Murinae; Mus.		
NCBI_TaxID=1090;		
SEQUENCE FROM N.A.		
STRAIN-C57BL/6J; TISSUE=Embryo;		
MEDLINE-A2351683; Published=12466851;		
The FANTOM Consortium,		
the RIKEN Genome Exploration Research Group Phase I & II Team;		
"Analysis of the mouse transcriptome based on functional annotation of		
60,770 full-length cDNAs."		
Nature 420:563-573 (2002).		
EMBL; AX034736; BAC28813.1; -.		
Hypotheoretical protein.		
NON_TER 1 1		
SEQUENCE 355 AA; 41315 MW; 93B39B4C82F86DD1 CRC64;		
QY 641 TRIKHCTPDSNIVNWFNWKAFFDEERARLQFYTGSSSRYPLQGKALQAGGPRFTI 700		
Db 1 RDDITLQINPDSAVNPEHLSYHFGIMAVFHRYIDGGFTLPFYKOLLGKSITLD 60		
QY 521 DMELYDPDLHSYLWILENDITGYLDHTFCVHNAYGBIOHELKENGKS.PVNNE 580		
Db 61 DMELYDPDLHSYLWILENDITGYLDHTFCVHNAYGBIOHELKENGKS.PVNNE 580		
QY 581 YVRLVNNWFLRGIAOFALQGFNEYIPQHLLKTDEKELEELIICGLGKIDVNDWKV 640		
Db 121 YVRLVNNWFLRGIAOFALQGFNEYIPQHLLKTDEKELEELIICGLGKIDVNDWKV 180		
QY 681 YVRLVNNWFLRGIAOFALQGFNEYIPQHLLKTDEKELEELIICGLGKIDVNDWKV 180		
Db 181 TRIKHTCPDSNIVNWFNWKAFFDEERARLQFYTGSSSRYPLQGKALQAGGPRFTI 240		
QY 701 HQIDACTNNLPAKTCFRIDIPPYESEKLYELVLTAEETCGFAVE 748		
Db 241 HQIDACTNNLPAKTCFRIDIPPYESEKLYELVLTAEETCGFAVE 288		
Q97 VSREEEIFEESYQTMKMRPKDLWKRLMIKFRGEEGLDYGGVAREWLYLICHEMNPYYGL 456		





		SQ	SEQUENCE	295 AA;	34030 MW;	0507325127A943EA	CRC64;
2	249 FRSRHHTEEDLEBEPESEGDVPEPWET-ISEBEVNLAGDSGLAPPPASPGRSTSPQL 307		Query Match Score: 1379; DB 4;	Length: 295;			
2	228 -----LAER-----RVRS-----QERNYNSRTHHEPDGL 253		Best Local Similarity: 34.2%; Pred. No. 2, 7e-99;				
2	308 SEBLRSRLQITDPSNGEQFSSLIQREFFSSRRCSVTTDAVEQGLPPSSVAVHTTQL 367		Matches 251; Conservative 24; Mismatches 19; Indels 0; Gaps 0;				
2	254 PEGYEQRITQQGQVYFLHQTGVSTWHDPL 288	Qy	455 GLFOVSRRDDITYLQINPDAVNPDEHLSYFHVFGRIMMAVPGKHYIDGGFTLPFYKQLLG 514				
2	368 PSSEWEERKDAKERTYYNNRRTTWTRPIMQLAEDGASSATANSNNHLIEPQIRPSSL 427	Db	2 GFEQYSTDNLYMLQINPDSINDHLSYFHVFGRIMLAVFHQHYINGFTPVYKQLLG 61				
2	289 SNTCEBGP-----LPGWEIRN 307	Qy	515 KSTITDDMELYDPDLHNSLWILENDITGVLDHTFCYEBNAHYGEILOHELPKNGKSLIPVN 574				
2	428 SSPTVTLAPSAGAKOSPVRAVQDTLSNPOSQPSPNSPKPKHQVTKTOSFLPGWENRI 487	Db	62 KPIQSLDBSVDPDLHKSJWILWENDITPVLDHTFCYEBNAGRILQHELPGRNVPT 121				
2	308 TATGRRYFEDVMDNRTTOFTDPPLSANTHLVNRQNOLKDQQQCVSICPDD----- 359	Qy	575 EENKEKEYVYLWNTRELEGIAEFLAQKGNEVIFPOHLKTDPEKEELIICLKIDV 634				
2	468 APNGRPFIDANTKTIWEDPRLKFVPHM-----RESTSINPNDLGPLPPGW 534	Db	122 EENKEKEYVYLWNTRELEGIAEFLAQKGNEVIFPOHLKTDPEKEELIICLKIDV 181				
2	360 -----TECLTVPR-YKBDLVQKLTKLROELSQQQPQ 389	Qy	635 NDWKUNTRLKHCTPDNSN1UKMFKAVEFDEERRARLQFTGSSRVPLOGKALOGAG 694				
2	535 EENHLDORTFTDHNSENKITOWEDPBLQNPATIGAVPSREFEQKYDFRKLIKPKADI 594	Db	182 NDWKUNTRLKHCTPDNSN1VRWFQAVEFDEERRARLQFTGSSRVPLOGKALOGAG 241				
2	390 AGHRRIESREEFEESYROMKMRPKDLW-RNLMKFRSEEGDLYGGVAREWLYLSSHE 448	Qy	695 PRLFTHQIDACTNNLPAKHTCNRDIPPYSSSYEKEYKLTAIBETCGFAVE 748				
2	595 PNRFEMKLHNRNFEEFSYRRLMSVKEFSEKGLDYGGAEEFLLSKE 654	Db	242 PRLFTHLIDANTDNLPKAHTCNRDIPPYSSSYELEYKLTAIBETCGFAVE 295				
			RESULT 10				
		Q9CSE3	PRELIMINARY;	PRT;	258 AA.		
		ID Q9CSE3					
		AC					
		DT 01-JUN-2001	(TREMBLre1. 17, Created)				
		DT 01-JUN-2001	(TREMBLre1. 17, Last sequence update)				
		DE 21.04.11 2002 (TREMBLre1. 21, Last annotation update)					
		GN 2810411E2R2IK.					
		OS Mys musculus (Mouse)					
		OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.					
		OX Nikaido I., Mashima J., Mazzarelli J., Mombaerts P., RN [1]					
		RP SEQUENCE FROM N.A.					
		RC MEDLINE=21083660; Published=11217851;					
		RC SEQUENCE=C57BL/6J; TISSUE=Embryo;					
		RA Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y., RA Akizawa K., Hara A., Nishi K., Kiyosawa H., Kondo S., Adachi J., Fukuda S., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kadota K., Matsuda H. A., Ashburner M., Batyalov S., Casavant T., RA Fleschmann W., Gaasterland T., Gissi C., Kochiwa H., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L. M., Staubli P., Suzuki R., Tomita M., Wagner J., Wastio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G., RA Blake J., Boiffelli D., Botunga N., Carninci P., de Bonaldo M.F., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Nordone P., Ring B., Rodriguez J., Sakamoto N., RA Sasaki H., Sato K., Schoenbach C., Suya T., Storch K.-F., RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilmung L., RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., RA Hayashizaki Y., RT "Functional annotation of a full-length mouse cDNA collection.", RL Nature 409:655-650 (2001).					
		DR EMBL; AK013082; BAB28637.1;					
		DR MGDB; MGI:193563; 2810411E2R2IK.					
		DR InterPro; IPR005659; HECT_domain.					
		DR Pfam; PF00632; HBCT_1.					
		DR SMART; SM00119; HECTC_1.					
		DR PROSITE; PS50237; HECT_1.					
		FT NON_TER 1 1					
		SQ SEQUENCE FROM N.A.					
		TISUB=Brain;					
		Wambutt R., Heubner D., Newes H.W., Gassenhuber J., Wiemann S.; Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.					
		EMBL; AL834242; CAD38919.1; -					
		InterPro; IPR000569; HECT_domain.					
		Pfam; PF00632; HBCT_1.					
		SMART; SM00119; HECTC_1.					
		PROSITE; PS50237; HECT_1.					
		HYPOTHETICAL protein.					
		NON_TER 1 1					
		SEQUENCE 258 AA;					
		SG SEQUENCE 29670 MW;					
		B0B04BCB1PCBC98 CRC64;					



The FANTOM Consortium,  
the RIKEN Genome Exploration Research Group Phase I & II Team;  
"Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.",  
Nature 20; 563-573 (2002).  
EMBL: AK086620; BAC0458\_1; -;  
EMBL: AK088767; BAC0558\_1; -;  
SGC:ENTREZ: 887; AA: 1023765; MM: 28733563386550; CDCC6;

RESULT 1



Ligase-  
SEQUENCE 854 AA; 981.81 MW; 00C74E1661F52E7P CRC64;  
 Query Match 33.5%; Score 1354.5; DB 4; Length 854;  
 Best Local Similarity 43.7%; Pred. No. 9.9e-97;  
 Matches 280; Conservative 98; Mismatches 200; Indels 63; Gaps 13;  
 Matches 280; Conservative 98; Mismatches 200; Indels 63; Gaps 13;

137 QSRDRIGTEQQVWDCSRLFDN--DLPGWEEERTASGRIQYLNHTRTOWERPRPAS 193  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 241 RARSSTVIGEEPITPSAVAVHTTPGLPSGWEEKRDAKRTYVNNHNRRTWTRIMQLA 300  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 194 EYSSPG-----REPLSC---FVIDENTPISTGNGATCGOSSDPRLAERRVS 235  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 301 EDGAGSGSATNSNNHLEPQIIRRSLSSPTVTLSAPLEGAKSDSPVRAVKDTLSNPSPQ 360  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 236 QRHNMYSRTHLHTPDLBEGYDORTIOQGVYQFLHQTCYSTWHBPRVP----RDLSN 290  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 361 PSPTNSPKPQKHVUTQSFLPGWENRJAPNGRPFIIDENTKTTWDERPLKPPVHRSKTS 420  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 291 INCEELGPAPPGEWTRNTATGRYVFDINNRTQFTPELRSANLHLVLTANONQLKDQQQ 350  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 421 LNPNLGPFLPPGWEERIHLDGRTFYIDENSKTQWEPRL-----QN----- 462  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 351 QVVSICLPPDDTECHVPR--YKRDLVQKURKILQBLSOOPQAGHCIEVSSEEIFPESYR 408  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 463 -----PATIGPAVPSREFKQKYDFRKKKPADIPNRFEMKLHRNNIFESTR 512  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 409 QVMQRKPDWK-RLMIKERGEBOLDYQGVAEFLYLISHENLNPyGLPFSRDIYTL 467  
 :|:|:|:|:|:|:|:|:|:|:|:  
 513 RIMSKTKRDPVTKARWIEFESERKGLDQGVAEWFWFLISKENFNPyGLPFSADNTYTL 572  
 :|:|:|:|:|:|:|:|:|:  
 468 QINPDSAV-NPEHLSYFHPTGRIMGMAVFGHYIDGGFTLPYKOLIGKSSTLDDMELVD 526  
 :|:|:|:|:|:|:|:|:|:  
 573 QINPAGLNEDEHSISYFTPIGRAGLAYFRGKLDGFIRPYKOMNLGKQTTLNDEMSVD 632  
 :|:|:|:|:|:|:|:|:  
 527 PDLHNSLWTLENDITGVLDTDHTPCVHNAYGEIQLHKLPGKSIPIVNEENKCYTRLY 586  
 :|:|:|:|:|:|:|:|:  
 633 SEYNNLSKWLLENPT-EUDLMRCIDEENFGOTYQVDLKPGSEIVNTVNKREYDVLVI 691  
 :|:|:|:|:|:|:|:  
 587 NWFRGIGIAQFLAQKGNEVIFQHLLKTFDEKELELJICLGKDNDKVNTRLK-- 644  
 :|:|:|:|:|:|:|:  
 692 QWRFTAVRQKQMNAAFLGETTELLPIDLJKIDENELBLLMCGLGDDVNDKWHSTYKNG 751  
 :|:|:|:|:|:|:|:  
 645 HCTPPSNIVKWFKAVEEFFDEERRARLQFVTGSSRYPLQGFKAQDGAAGPRLFTHQID 704  
 :|:|:|:|:|:|:|:  
 752 YC-PHPVQOWFNAVLLMDAERBLIQFVTGSSRYPLQGFKAQDGAAGPRLFTHQID 810  
 :|:|:|:|:|:|:  
 705 ACTNOLPKRAHTCFNRIDIPYSESYKYEKLTAIEETCGF 745  
 :|:|:|:|:|:|:  
 811 S-PEKLPRAHTCFNRLDLPYEFEDLSREKLIMAVENAQGF 850



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			301 PGWEIRNTATGRVYFYDHNRRTOFTDPLRSANHLVLRNQNLXRDQQCCQYVSLCPDDT 360
		Qy	301 PGWEIRNTATGRVYFYDHNRRTOFTDPLRSANHLVLRNQNLXRDQQCCQYVSLCPDDT 360
		Db	361 ECITVPRYCRDLVQLKLRQELSQQQPQAGHRIVSREEFEEYSYRQMKMRPKDLWK 420
		Qy	361 ECITVPRYCRDLVQLKLRQELSQQQPQAGHRIVSREEFEEYSYRQMKMRPKDLWK 420
		Db	421 RLMIKPBRGEGLDGGCAREWYLISHEMLNYGYLQYSRSDDIYLTQINPSAQNPEHL 480
		Qy	421 RLMIKPBRGEGLDGGCAREWYLISHEMLNYGYLQYSRSDDIYLTQINPSAQNPEHL 480
		Db	481 SYFHVGRIMGMAVFQHGYIDGFTLPYKQJLGKSITLDMDLVDPDLANSVLNLEND 540
		Qy	481 SYFHVGRIMGMAVFQHGYIDGFTLPYKQJLGKSITLDMDLVDPDLANSVLNLEND 540
		Db	541 ITGVLDLHTFCVENVAYGEIQLQHLPNERSIPIVNEENKEYVRLYNWRFLRGTEAQFLA 600
		Qy	541 ITGVLDLHTFCVENVAYGEIQLQHLPNERSIPIVNEENKEYVRLYNWRFLRGTEAQFLA 600
		Db	541 ITGVLDLHTFCVENVAYGEIQLQHLPNERSIPIVNEENKEYVRLYNWRFLRGTEAQFLA 600
		Qy	601 LQKGFEVIPQHLLKTFDEKELELIICGLGDVNDKVNTRLKHTCPDSNTVKNEWKAV 660
		Db	601 LQKGFEVIPQHLLKTFDEKELELIICGLGDVNDKVNTRLKHTCPDSNTVKNEWKAV 660
		Qy	661 EFDDEBARRLQLQFTGSSRPVQGKFALQGAAGPRLFTHQIDACTNNLPKAHTCFNRI 720
		Db	661 EFDDEBARRLQLQFTGSSRPVQGKFALQGAAGPRLFTHQIDACTNNLPKAHTCFNRI 720
		Qy	721 DIPPYESYKLYEKULATAEETCGFAVE 748
		Db	721 DIPPYESYKLYEKULATAEETCGFAVE 748
		RESULT 2	
		SUFI_HUMAN STANDARD; PRT; 757 AA.	
		ID_SUP1_HUMAN STANDARD; PRT; 757 AA.	
		AC Q9RCE7; O75853; STANDARD; PRT; 757 AA.	
		DT 28-FEB-2003 (Rel. 41; Created)	
		DT 28-FEB-2003 (Rel. 41; Last sequence update)	
		DT 28-FEB-2003 (Rel. 41; Last annotation update)	
		DB Smad ubiquitination regulatory factor 1 (EC 6.3.2.-) (Ubiquitin-DE protein ligase SMURF1) (Smad-specific E3 ubiquitin ligase 1) (SMURF1)	
		DE DE	
		GN SMURF1 OR KIAA1625.	
		OS Homo sapiens (Human).	
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
		RN [1] _TAXID=9606;	
		RP SEQUENCE OF 10-731 FROM N.A. (ISOFORM SHORT).	
		RA MEDLINE=9385348; PubMed=1045816;	
		RT "A SMAD ubiquitin ligase targets the BMP pathway and affects embryonic pattern formation."	
		RL Nature 400:687-693 (1999).	
		RP SEQUENCE OF 20-731 FROM N.A. (ISOFORM SHORT).	
		RA Stomskiing T.; Bauer C.; O'Neal D.;	
		RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.	
		RN [2] _SEQUENCE FROM N.A. (ISOFORM LONG).	
		RP SEQUENCE FROM N.A. (ISOFORM LONG).	
		RC TISSUE=Brain;	
		RX MEDLINE=20450683; PubMed=10997877;	
		RA Nagase T.; Kikuno R.; Nakayama M.; Hiroseawa M.; Ohara O.;	
		RT "Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."	
		RL Res. 7:273-281(2000).	
		CC FUNCTION: INTERACTS WITH RECEPTOR-REGULATED SMADS SPECIFIC FOR THE BMP PATHWAY (SMAD1 AND SMAD5) IN ORDER TO TRIGGER THEIR INACTIVATION.	
		CC UBIQUITINATION AND DEGRADATION AND HENCE THEIR INACTIVATION.	
		CC - ALTERNATIVE PRODUCTS:	
		Event=Alternative splicing; Named isoforms=2;	

Name=Long;				
Isord=9HQB7-1; Sequence=Displayed;				
Name=Short;				
- - Isord=9HQB7-2; Sequence=VSP_006812;				
- - SIMILARITY: Contains 1 C2 domain.				
- - SIMILARITY: Contains 2 WW domains.				
- - SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.				
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EMBL; AEI99364; AAFF08298_2; -.				
EMBL; AB046845; AAC2434_1; -.				
EMBL; BAB13451_1; ALT_INIT.				
HSSP; Q13526; 1PIN.				
MM; 605568; -.				
GO; GO:0005622; C:intracellular; TAS.				
GO; GO:000211; F:protein degradation, tagging activity; IDA.				
GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.				
GO; GO:0030154; F:cell differentiation; IDA.				
GO; GO:0039208; P:ectoderm development; TAS.				
GO; GO:000514; P:negative regulation of BMP signaling pathway; TAS.				
GO; GO:0006464; P:protein modification; TAS.				
SMART; SMART_00612; P:ubiquitin cycle; IDA.				
InterPro; IPR000009; C2.				
InterPro; IPR0000569; HECT domain.				
InterPro; IPR001202; WW_Rsp5_WWP.				
Pfam; PF00168; C2_1.				
Pfam; PF00632; HECT_1.				
SMART; SMART_00239; C2_2.				
SMART; SMART_00119; HECTC_1.				
PROSITE; PS00490; C2_DOMAIN_1.				
PROSITE; PS50004; C2_DOMAIN_2; 1.				
PROSITE; PS50237; HECT_1.				
PROSITE; PS01159; WW DOMAIN_1; 1.				
PROSITE; PS50020; WW DOMAIN_2; 2.				
Ub1 conjugation pathway; Ligase; Repeat; Alternative splicing.				
DOMAIN 1 99 C-> LIGASE; Repeat; Alternative splicing.				
DOMAIN 267 WW 1.				
DOMAIN 339 WW 2.				
DOMAIN 757 HECT.				
BINDING 725 UBIQUITIN.				
VARSPIC 294 Missing (in isoform Short).				
MUTAGEN 725 /FTD=vsp 006812.				
SEQUENCE 757 AA; 86113 MW; 892171CF4B40E5 CRC64; C-> LOSS OF UBIQUITINATION CAPACITY.				
Query Match 74.7%; Score 3015.5; DB 1; Length 757;				
Best Local Similarity 72.2%; Pred. No. 7e-208; Matches 63; Mismatches 73; Indels 85; Gaps 10;				
MatcheS 574; Conservative 72.2%; Pred. No. 7e-208; Matches 63; Mismatches 73; Indels 85; Gaps 10;				
SEQUENCE 757 AA; 86113 MW; 892171CF4B40E5 CRC64;				
1 MSNPGRERRNG-PVKURLTVLCAKNIYKQDFERFLPDPFKAIVYDGGSOCHSTDFTVKTLDP 59				
1 MSNPGRERRNGSIKRLTVLCAKNAKDFERFLPDPFKAIVYDGGSOCHSTDFTVKTLDP 60				
60 KWNQHYDLYIKGKSDSVTISWNHKKIKHKQOGFLGCYRLLSNAINBLKQGYQRDLCK 119				
61 KWNQHYDLYIKGKSDSVTISWNHKKIKHKQOGFLGCYRLLSNAINBLKQGYQRDLCK 120				
120 LGPNNDTWRQIVVLSQEDRIGTGQVWDGSRPLDPCWEERTASGRQLNHI 179				
121 LNPSDIDAVRGQIVVLSQEDRIGGGSTVDCGLLENB-----GTYY---- 163				
180 TRTTQMERPTPRASSYSPRPRLFCVDENTPISGTGATCG-----QSSDPRLAE 230				

164 -----EDSGPGRPLSCMEEPAVYDSTGAACGGNCRCFVEPSQDQRLQA 209  
 QY :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:  
 Db 231 RYRSQRHRYM---SRTHLITPPDPEGEQRTTOQQVIFLQTGQYSTMDPRV-- 284  
 Db 210 QRLNPDVGSLOTPQRPHQSQSPLEPGYEQRTVQGVYFHTQGYSWTMDPRIPS 269  
 285 -----PRDLNNINCEELGPPLPGWETRNTATGRVYFVDHN 320  
 Db 270 PGSTIPGGDAATLYEPFLQGHSTSEPDLSNSCDEGPPLPGWETRSTVSPRIEVDRN 329  
 Db 321 RTQFTDRLSANLHLVLRNQLQDQQQCVV---SLCPDDTECLTVRYKRDVLQKL 376  
 Db 330 RTQFTDR---LHHMMAHQCQLKEPSQPPLPSGSL---EDSELPAQYERDVLQKL 382  
 377 KILRQELOLSCOOPOAGHCRIEVSREEFEESTYRQVMKRPKDLMTRMLMIKPRGEFGLDYGG 436  
 Db 383 KVURHELSLQQPAGHCRIEVSREEFEESTYRQVMKRPKDLMVRGEFGLDYGG 442  
 QY 437 VAREWLYLJSHMLNPYPGLFOYSRDIYLQINPDSAYVNPEHLSYFHVGRINGMAVEH 496  
 Db 443 VAREWLYLJLCHENLNPyGLFOYSTDNYLQINPNSSTNDHLSYFHVGRINGLAVFH 502  
 QY 497 GHYDGGFTLPYKQKGKSITUDDMELVPPDHLNSLWILENDITGULDHTFCYERNAY 556  
 Db 503 GHYTNGGTPVPPFKQOLGKPTQLSOLESDVDEBLHSLSLWILENDITPVLDHTFCYEHNAF 562  
 QY 557 GEI1QHEKPKNGKSIPYVNEENKEYVRLYVAWFPLRGIEQFLALQKGNEVIQHLLKT 616  
 Db 563 GRILQHEKPKNGSIPYVTEENKKEYTRLYVNWFRYFQFLALQKGNEVIQHLLKT 622  
 QY 617 FDKEKELELIGGKEDVNDWVNTLKHCTPDNSIVKWFVKAVFFFDEERARLQFVT 676  
 Db 623 FDQXKELELIGGKEDVNDWVNTLKHCTPDNSIVKWFVKAVFFFDEERARLQFVT 682  
 QY 677 GSVRPVPGOFKALQ---GAAGEBRLFTIHOIDACTNLPKAHTCFNRIDIPPYESYEKLYE 733  
 Db 683 GSVRPVPGOFKALQGSTGAAPRLFTIHDANTDNLPKAHTCFNRIDIPPYESYEKLYE 742  
 QY 734 KLTIAIEETCGFAVE 748  
 Db 743 KLTIAIEETCGFAVE 757

## RESULT 3

SUFI\_XENIA STANDARD; PRT; 731 AA.

ID SUFI\_XENIA STANDARD; PRT; 731 AA.

AC Q9P012; Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Smad ubiquitination regulatory factor 1 (EC 6.3.2.-) (Ubiquitin-)

DE protein ligase SMURF1 (Smad-specific E3 ubiquitin ligase) (xSMURF1).

GN SMURF1. Xenopus (African clawed frog).

OS Xenopus laevis (Clawed frog).

OC Eukaryota; Metacozoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

OC Xenopodinae; Xenopus.

NCBI TaxID=3355; [1]

RN [1]

RP Sequence from N.A.

RC Tissue=Larval;

RX MEDLINE=9935348; PubMed=10458166;

RA Zhu H., Kavak P., Abdollah S., Wana J.L., Thomsen G.H./

RT "A SMAD ubiquitin ligase targets the BMP pathway and affects embryonic pattern formation.";

RT RL Nature 40:687-693 (1999).

-4 FUNCTION: INTERACTS WITH RECEPTOR-REGULATED SMADS SPECIFIC FOR THE BMP PATHWAY (SMAD1 AND SMAD5) IN ORDER TO TRIGGER THEIR UBIQUITINATION AND DEGRADATION AND HENCE THEIR INACTIVATION. MAY REGULATE ECTODERMAL DIFFERENTIATION AND PATTERN BY MODULATING BMP SIGNALING AND MAY ENHANCE CELLLULAR RESPONSIVENESS TO THE SMAD2 (ACTIVIN/TGF BETA) PATHWAY.

-1 DEVELOPMENTAL STAGE: EXPRESSED FROM THE EGG STAGE TO THE SWIMMING

TADPOLE, WITH MAXIMUM LEVELS OBSERVED IN THE STAGES FROM EGG TO GASTRULA. AT GASTRULATION DISTRIBUTED UNIFORMLY IN EMBRYONIC ECTODERM AND INVOLVING MESODERM, AND EXPRESSION GRADUALLY LOCALIZES TO THE NERVOUS SYSTEM. AT EARLY TADPOLE STAGES EXPRESSED IN THE CNS, EYE, BRANCHIAL ARCHES, KIDNEY AND SOMITES.

-|- SIMILARITY: Contains 1 C2 domain.

-|- SIMILARITY: Contains 2 WW domains.

-|- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.

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EMBL; AF16931; PF005622; Cintzecellular; TAS.  
 GO; GO:0002111; Protein degradation, tagging activity; IDA.  
 GO; GO:0004561; Ubiquitin-protein ligase activity; IDA.  
 GO; GO:003154; Protein degradation; IDA.  
 GO; GO:0007399; Plectoderm development; TAS.  
 GO; GO:0006456; Negative regulation of BMP signaling pathway; TAS.  
 GO; GO:0006514; Ubiquitin cycle; IDA.  
 InterPro; IPR000008; C2 domain.  
 InterPro; IPR000569; HECT domain.  
 InterPro; IPR001202; WW\_Rsp5\_WWP.  
 Pfam; PF00168; C2; 1.  
 Pfam; PF00632; HECT; 1.  
 Pfam; PF00397; WW; 2.  
 SMART; SMC023; C2; 1.  
 SMART; SMC011; HECT; 1.  
 SMART; SMC0456; WW; 2.  
 PROSITE; PS00099; C2\_DOMAIN\_1; 1.  
 PROSITE; PS50004; C2\_DOMAIN\_2; 1.  
 PROSITE; PS50237; HECT; 1.  
 PROSITE; PS01159; WW\_DOMAIN\_1; 1.  
 PROSITE; PS50200; WW\_DOMAIN\_2; 2.  
 Ubl conjugation pathway; Ligase; Repeat DOMAIN.  
 DOMAIN 1 99 C2 DOMAIN.  
 DOMAIN 233 266 WW 1.  
 DOMAIN 394 312 WW 2.  
 DOMAIN 731 AA; 83299 MW; 3C888E512A42CE2C2 CR064;

Query Match 72.7%; Score: 2937.5; DB: 1; Length: 731;

Best Local Similarity 72.7%; Pred. No. 2.5e-202; Matches 558; Conservative 68; Mismatches 85; Indels 57; Gaps 9;

1 MSNPGRNG-PVKRLRTVLCANLWKKDFERFLDPFKAKVYDGSQGCHSDPTVNLTD 59  
 1 MSNVTRRGSSIRVLTIVCAKLWKKDFERFLDPFKAKVYDGSQGCHSDPTVNLTD 60  
 60 KRNQHDLYIGKSDSVTISWNHKKTHKKQAGFLGCCRLSNAINRLKDQYQRLDCK 119  
 61 KRNQHDLYGKMDITISWNHKKTHKKQAGFLGCCRLSNAISRLKDQYQRLDCK 120  
 120 LGPNNDTDTGQIVVSLQSQRDRTGQVQDCSRLFDNDLDPGEERRTAGRIQWLNI 179  
 121 LNPTNDDAVRQIVVSLQFEDRIGLGSVDCLGLDN-----GAL----- 162  
 180 TRTTOVERPRTPASVYSSPQRPLSFVDTNPI-----STNGATGQOSDPLAERVRSQ 236  
 163 -----LEDTGPORPLSOMDDEPAFPTDGAAGGSPRLVYESPQEQLQQA 209  
 237 RHRNTMSRTHLTP-----PLDPEXYORTQOCQVYFLHTCTGVSYWHDPYRVD 287  
 210 RVRGPEYEHQTPNRSHFQSQULPEGYEQRTVQVYFLHTQGVSWHDPPIRD 269  
 288 LSNNIEELGLPPIPWEIRNTATGRVYFDHNRRTTQFTDPLSANLHLVNRQQLKDQ 347

RESULT 4  
 SURF\_MOUSE STANDARD PRTR; 619 AA.  
 ID SURF\_MOUSE STANDARD PRTR;  
 AC Q5CUN6;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Smad ubiquitination regulatory factor 1 (EC 6.3.2.1) (Ubiquitin--protein ligase SMURF1) (Smad-specific E3 ubiquitin ligase 1)  
 DE (Fragment).  
 GN SMURF1.  
 OS Mus musculus (Mouse).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Rutherford; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N A.  
 RC SPAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=21085660; PubMed=1121851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Niishi K., Kiyosawa H., Kondo S., Yamamoto T., Saito T., Okazaki T., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H., Ashburner M., Battalov S., Casavant T., Pleischmann W., Gaasterland T., Gissi C., King B., Kohchiwa H., Kuchi P., Lewis S., Matsuoka Y., Nakaido I., Pesole G., Quackenbush J., Staubli L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.P., Brownstein M.J., Bult C., Fleicher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Schoenbach C., Seya T., Shabata Y., Storch K.-F., Sasaki H., Sato K., Schoenbach C., Seya T., Shabata Y., Storch K.-F., Shizuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wimring L., Wynshaw-Boris A., Yoshida K., Hassegawa Y., Kawai H., Kohsuki S., Hayashizaki Y.;  
 RA Functional annotation of a full-length mouse cDNA collection.;  
 RT Nature 409:685-690 (2001).  
 RL -!- FUNCTION: interacts with receptor-regulated SMADs specific for the BMP pathway (SMAD1 and SMAD5) in order to trigger their CC

## UBIQUITINATION AND DEGRADATION AND HENCE THEIR INACTIVATION (By

-|- SIMILARITY: Contains 1 C2 domain.  
-|- SIMILARITY: Contains 2 WW domains.

-|- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.

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HSSP; Q13526; 1PIN; MGD; MG1:1.923038; 4930431E05ik.

GO; GO:0000211; C:intracellular; ISS.

GO; GO:0000211; F:Protein degradation, tagging activity; ISS.

GO; GO:0004842; F:Ubiquitin-protein ligase activity; ISS.

GO; GO:000154; P:cell differentiation; ISS.

GO; GO:00030514; P:ectoderm development; ISS.

GO; GO:0006464; P:negative regulation of BMP signaling pathway; ISS.

InterPro; IPR000008; C2.

InterPro; IPR000159; HECT domain.

InterPro; IPR0001202; WW\_Rsp5\_WWP.

Pfam; PF00397; HECT; 1.

Pfam; PF00397; WW; 2.

SMART; SM00119; HECTC; 1.

SMART; SM00456; WW; 2.

PROSITE; PS00599; C2\_DOMAIN\_1; PARTIAL.

PROSITE; PS50064; C2\_DOMAIN\_2; PARTIAL.

PROSITE; PS50337; HECT; 1.

PROSITE; PS01159; WW\_DOMAIN\_1; 1.

PROSITE; PS50020; WW\_DOMAIN\_2; 1.

Ubl conjugation pathway; Ligase; Repeat.

NON\_TER; 1

DOMAIN; 125 158 WW 1.

DOMAIN; 171 204 WW 2.

DOMAIN; 285 619 HECT.

DOMAIN; 35 38 POLY-GLY.

SEQUENCE; 619 AA; 70902 MW; 4CBE2F8624A7B525 CRC64;

1 DTGYQLDCKLQNLHITRTQWERPTRPASEYSSPGRPLSCFVDTENTPISTGNTATCG-----

50 VSRDIDPVRDLSMINCELGFLPGMEIRNTATGRYFDHANNRTQFDPLSLNHL-----

150 VSTWEDPRDLSVNCDELGFLPGMEVRSTSGRLYFVDHNNTTQFDPLR---LH 205

169 ASGRIQLNHITRTQWERPTRPASEYSSPGRPLSCFVDTENTPISTGNTATCG-----

221 51 -GTY------EDSGPGRPLSCMEEPAVTDGTAGGGNCRFV 89

222 -QSDFPRLAERYTSQRERNM---SRTHTHTPPOLPEGTYQRTQGQYYELHTQTG 275

90 BPSQNQRLVQRLNPBVGQPLQTPQRPHQSPSEPEGYQRTQGQYYELHTQTG 149

276 VSTWEDPRVPRDLSMINCELGFLPGMEIRNTATGRYFDHANNRTQFDPLSLNHL 335

150 VSTWEDPRDLSVNCDELGFLPGMEVRSTSGRLYFVDHNNTTQFDPLR---LH 205

336 LVLNQNQLKDDQQ-QVYSLCPDDTECLTVPPYKRDIVQKULIQLQELSQQPQGHCR 394

206 HMMERCOLKEPSQFLQPNEGSYDEELPAQYERDVQVKVLHELSLQQPQGHCR 265

395 IEVSSEEIEFSYRVMKRPDKWIKRUMIKRIFGEGLDGYGVVARWLYLISHEMINPYY 454

266 IEVSSEEIEFSYRQMCRPADLKRMVKFRGEGLDGYGVVARWLYLICHENINPYY 325

QY	455 GLFOYSRDDIYTQINPDSAYNPPEHLSYFHTYGRIMGMAYFHGHYIDGCFTLPPFKQKLG 514
Db	326 GLFOYSTNTIYTQINPDSAINPDHSYFHVGRMLGAFTGHAYINGGTFVTPYKQKLG 385
Qy	515 KSTLDDMELVDDPLANSLWLENDITGVLDTFCEVERDAYGEIQLHELPNGKSIIPVN 574
Db	386 KPIQSDLESVPBLHSLSLWLENITPVLDLHTFCEVERDNAFGRLQHELPNGRNVPVT 445
Qy	575 EENKEKYVRLYNNWRURGIEQFLAQKGNEVTFQHLLRTFDERELEJICGHGKIDV 634
Db	446 EENKEKYVRLYNNWRURGIEQFLAQKGNEVTFQHLLRTFDERELEJICGHGKIDL 505
Qy	635 NDWVNTNLKHCTPDNSIVKNEWKAEFFDERARLLOVTTGSRRVPLQGFKAQOGAQ 694
Db	506 NDWSNTNLKHCUADSIVRNWQAETFDERARLLOVTTGSRRVPLQGFKAQOGAQ 565
Qy	695 PRLFTHOIDACTNPLKAHTCNFRNDIPPYESKLYKEKLTALETGCFAVE 748
Db	566 PRLFTHIDANTDNPLKAHTCNFRNDIPPYESKLYKEKLTAVEETCGFAVE 619
RESULT 5	
PUBLI_SCHPO	ID_PUB1_SCHPO STANDARD; PRT; 767 AA.
AC	Q92462; O14454; Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ubiquitin--protein ligase publ (EC 6.3.2.-).
GN	PUBLI_OR SPAC11G7_02.
OS	Schizosaccharomyces pombe (Fission Yeast).
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomyces;
OC	Schizosaccharomyces pombe; Schizosaccharomyces.
OC	NCBI_TAXID=1896;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96205868; PubMed=8635463;
RA	Narabay B., Beach D.;
RT	"Publ acts as an E6-AP-like protein ubiquitin ligase in the degradation of cdc25."
RL	EMBO J. 15:1301-1312(1996).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=J227; RC
RX	MEDLINE=97340937; PubMed=9197411;
RA	Seguroo J., Peat N., Karagiannis J., Young P.G.;
RA	"Tolerance of low pH in Schizosaccharomyces pombe requires a function Publ ubiquitin ligase.";
RL	MOI. GEN. 254:520-528(1997).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=972; RC
RX	MEDLINE=21848401; PubMed=11859360;
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Baker S., Bowman S., Churcher C.M., Brooks K., Brown D., Brown S., Chillingworth T., Davies P., Fallwell T., Hamlin N., Hayles D., Hidalgo J., Hodson G., Collins M., Connor R., Cronin A., Davis P., Fallwell T., Goble A., Hamlin N., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., Holroyd S., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moulie S., Munzall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Robbins K., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Simmonds M., Squares R., Stevens K., Steerton J., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Taylor K., Volickaert G., Aert R., Robben J., Grimonpre B., Waltjens I., Vanstreels E., Rieger M., Scheffer M., Mueller-Auer S., Gabel C., Fuchs C., Holzer B., Noesti D., Hilbert H., Borzym K., Langner I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler R., Wambutt R., Burnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Leilaure V., Mottier S.,

Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G., Daga P.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The Genome sequence of Schizosaccharomyces pombe.",	Db	56 WNETFEVNVTDNSTIAQVEDOKF-KKKGGFGFLGYINLRGVDDLDLAIIGGDENLTRDLK 114
-!- FUNCTION: REGULATES UBIQUITINATION OF CDC25.	Qy	119 KLGENDNDTVERGQIVVSLQ----- 137
-!- CATALYTIC ACTIVITY: AMP + ubiquitin + protein lysine = AMP + diphosphate + protein-N-ubiquityllysine.	Db	115 K--SNVENTVHGMIIINISTAQSTLQPSSAAGGARTQETSIINDPOSSQSSSVSRNPA 172
-!- MISCELLANEOUS: A cysteine residue is required for ubiquitin-thiolester formation.	Qy	138 -----SRLRGWBERTASGRTOYLHITRTRQ 184
-!- SIMILARITY: Contains 1 C2 domain.	Db	173 SRRAGSPTRDNAPAAASSEPRTFESSEDYGRGPWGWRTRDNLGRTYVDNTRSIT 232
-!- SIMILARITY: Contains 3 WW domains.	Qy	185 WERTP-----RPASEYSSPGRPLSFVDFDENTPISTGNTGATCGQSSDPLAERRVRQRH 238
-!- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.	Db	233 WIRPNLSSVAGAAAELHSSA--SANTEGVQPPSSNAA-----RTEASVLT--- 279
-!- SIMILARITY: STRONG, TO YEAST RSP5.	Qy	239 RNTMSRTLHTTPDLPGLPGYEQTQGQVYPLHTQGVSHTHDPVRVPLDSNIN----- 292
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EMBL; Q13526; SPAC11G.02; -.	Qy	293 -----CEELGPLEPGWEIWTNPATGTYFDINNRTQFDPRLSANLHLVNRNQLKQ 347
EMBL; U66716; AAB07514.1; -.	Db	336 IQQQPVSQLCPDPLFGWMRLNTARYFEDNTKTWDPRLSSL-----DQ 384
EMBL; 299145; CAB16207.1; -.	Qy	348 QQQQVSQLCPDPLBCLTVPRYRDLVQKLRLQELSQQ -QPAQHCRIEVSEEEIFBS 405
PIR; S66562; S66562.	Db	385 -----NVPQTKRDPFRKLTYF--LSQPALHPLPGQCHIKVRAHNHFID 425
PIR; T37545; T37545.	Qy	406 SYRQYMKRKPDKLWKRMKIKPFGEGVARELYLISHEMLNPFYGLFOSRDDY 465
GenedB; SPombe; SPAC11G.02; -.	Db	426 SYA1MRSATDJKRMKIDPDKDGDYDGLSREYFFLUSHENPNFYLCEFSVVDNY 485
InterPro; IPR000008; C2.	Qy	466 TQINPDAVNPHLSYFHFGIMMAVEFGHYDGGFLPLPFYKQLGKSITLDDMELV 525
InterPro; IPR000569; HECT_domain.	Db	486 TLQINPHGINPFLNFKFGRVIGAIFFRYDAAFFVSFRMILRKVTQDMBNK 545
InterPro; IPR003349; WW.	Qy	526 DPDLHNSLWLENDTICVLQDHTFCYEHNMAYGEIQLHELKPGNGKSIPYNEENKEVYRL 585
InterPro; IPR001202; WW_Rsp5_WWP.	Db	546 DALEYTRSLWLUINDTCVLQDHTFSYDNCGEVYTIDAKPGNGNIEVTEENKEYVDLV 605
Pfam; PF00168; C2_1.	Qy	586 VNTFLRGLEAQQLALQKGFRNIVIPORLKLTFDELELLIGLCKIDNDWKNTRLK 645
Pfam; PF00632; HECT_1.	Db	606 TVVRIQRIEEQFNAPHEGFSLLIPQELINVFDELELLIGGISEIDMWKHTDRS 665
PRINTS; PRO00403; WDOMAIN.	Qy	646 CTPPSNITYKWNFAKVEFDEBRARLIQFTGTSRVSYVPLQGFKALOGAAGPLFLTHQIDA 705
SMART; SM00239; IC2_1.	Db	666 YSENQDQ1XKWFHLMDSNEKSKRLLQFTGTSRVPDNGSDPRKTTIEKAGE 725
SMART; SM00149; HECTC_1.	Qy	706 CTNNLPKAHTCFNRIDIPPYESKLYEKLTIAEFTCGFAVE 748
PROSITE; PS00049; C2_DOMAIN_1; 1.	Db	726 -PNKLPKAHTCFNRLDPPYTSKQDLDHKLISIAVEETIGFQE 767
PROSITE; PS50004; C2_DOMAIN_2; 1.	RESULT 6	
PROSITE; PS50237; HECT_1.	RSP5_YEAST	
PROSITE; PS01159; WW_DOMAIN_1; 3.	ID	
PROSITE; PS50020; WW_DOMAIN_2; 3.	AC	31, Created)
Ub1 conjugation pathway: Ligase; Repeat.	DT	01-FEB-1995 (Rel. 31, Last sequence update)
DOMAIN 17 32 C2 DOMAIN.	DT	15-SEP-2003 (Rel. 42, Last annotation update)
DOMAIN 21 236 WW 1.	DB	Ubiquitin- -protein ligase RSP5 (BC 6.3.-)
DOMAIN 242 247 POLY_ALA.	GN	RSP5 OR NPII OR MDPI OR YER125W OR SYGP-ORF1.
DOMAIN 294 319 WW 2.	OS	Saccharomyces cerevisiae (Baker's yeast)
DOMAIN 351 376 WW 3.	OC	Bakaryota; Fungi; Ascomycota; Saccharomyces; Saccharomyces
DOMAIN 463 767 HECT.	OC	Saccharomyces; Saccharomycetales; Saccharomycaceae; Saccharomyces
BINDING 735 735 UBIQUITIN (BY SIMILARITY).	OX	
CONFLICT 163 163 Q->K (IN REF. 1).	RN	
CONFLICT 609 609 MISSING (IN REF. 1).		
CONFLICT 661 661 T->K (IN REF. 1).		
SEQUENCE 767 AA; 87267 MW; F1155A155EBPACP7 CRC64;		
Query Match 39.3%; Score 1585.5; DB 1; Length 767;		
Best Local Similarity 41.3%; Pred. No. 1.3e-105;		
Matches 340; Conservative 121; Mrsmatches 231; Indels 131; Gaps 17;		
1 MSNPGRRNPGPKLRLTVCAKNUVKDFFRLPDPKAKVYDGSQGCHSTDTRVTKTLDPK 60		
1 MSNSAQR---RIRRIVADGLYKRDFERFPDFAVLTVDDB-QTHTTTAIKTLNPY 55		
61 WNOHYDLYIGKSDSUTISVNHKKHGAGFLGCVRLSNAINRLKDTGYQL--DLC 118		

Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Bostein D., Davis R.W.; "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome V."; Nature 387:78-81(1997). [2]

IDENTIFICATION.  
Winston F.; Unpublished observations (FEB-1993). [3]

CHARACTERIZATION.  
STRAIN=Sigma 1278B;  
MEDLINE=0615194; PubMed=8596462;

[4] Heim C., Haguenuauer-Tsapis R., Andre B.; "NP11, an essential yeast gene involved in induced degradation of Gap1 and Fur4 permeases, encodes the Reps ubiquitin-protein ligase."; Mol. Microbiol. 18:77-87 (1995).

FUNCTION  
MEDLINE=95223981; PubMed=7708685;  
Huizinga J.M., Scheffner M., Beaudenon S., Howley P.M.; "A family of proteins structurally and functionally related to the E6-AP ubiquitin-protein ligase."; Proc. Natl. Acad. Sci. U.S.A. 92:2563-2567 (1995). [5]

ERATUM.  
MEDLINE=95281634; PubMed=7761480;  
Huizinga J.M., Scheffner M., Beaudenon S., Howley P.M.; Proc. Natl. Acad. Sci. U.S.A. 92:5249-5249 (1995). [6]

CHARACTERIZATION.  
STRAIN=P56;  
MEDLINE=99077972; PubMed=9858558;  
Wang G., Yang J., Huibregtsse J.M.; "Functional domains of the rps5 ubiquitin-protein ligase."; Mol. Cell. Biol. 19:3422-352 (1999).  
- - FUNCTION: E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM AN E2 UBIQUITIN-CONjugating ENZYME IN THE FORM OF A THIOESTER AND THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATES REQUIRED FOR DEGRADATION AND THEREFORE DEGRADATION OF SEVERAL CELL SURFACE PROTEINS LIKE GAP1, FUR4, MAL1 AND ST2. ALSO ACTS ON RBE1.  
- - SUBCELLULAR LOCATION: Cytoplasmic and nuclear (Potential).  
- - PTM: THE UBIQUITINATION APPEARS TO BE THE RESULT OF AN INTRAMOLECULAR TRANSFER OF UBIQUITIN.  
- - MISCELLANEOUS: A cysteine residue is required for ubiquitin-thioester formation. Contains 1 C2 domain.  
- - SIMILARITY: Contains 3 WW domains.  
- - SIMILARITY: Contains 1 HBCT-type E3 ubiquitin-protein ligase.  
- - SIMILARITY: STRONG TO S. POMBE PUB1.  
- - SIMILARITY: TO YEAST YKL01C.

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EMBL: U19916; AAC03223.1; - .  
PIR: S43217; S43217.

HSSP: Q13526; 1PIN.  
SGD: S0000927; RSP5.

GO: GO-0000151; C:ubiquitin ligase complex; IDA.  
GO: GO-0005333; P:chromatin assembly/dissassembly; IDA.  
GO: GO-0005513; P:protein monoubiquitination; IDA.  
InterPro: IPR000008; C2.  
InterPro: IPR000008; C2.  
InterPro: IPR000569; HECT\_domain.

DR InterPro; IPR002349; WW.  
DR InterPro; IPR001202; WW\_Rsp5\_WWP.  
DR PROSITE; P900499; C2\_DOMAIN\_1;  
DR PROSITE; P850004; C2\_DOMAIN\_2;  
DR PROSITE; P850023; HECT\_1.  
DR PROSITE; PS01139; WW\_DOMAIN\_1;  
DR PROSITE; PS00020; WW\_DOMAIN\_3;  
DR SMART; SM00119; HECTC\_1.  
DR SMART; SM00456; WW\_3;  
DR PROSITE; P900499; C2\_DOMAIN\_1;  
DR PROSITE; P850004; C2\_DOMAIN\_2;  
DR PROSITE; P850023; HECT\_1.  
DR PROSITE; PS01139; WW\_DOMAIN\_1;  
DR PROSITE; PS00020; WW\_DOMAIN\_3;  
KW Ubl conjugation pathway Ligase; Repeat.  
FT DOMAIN 1 88 C2 DOMAIN.  
FT DOMAIN 229 262 WW 1.  
FT DOMAIN 315 322 POLY\_ALA.  
FT DOMAIN 331 364 WW 2.  
FT DOMAIN 387 420 WW 3.  
FT DOMAIN 705 809 HECT.  
FT BINDING 777 777 UBIQUITIN.  
FT VARIANT 733 733 L -> S (IN RSP5-1; IMPAIRED IN UBIQUITIN-THIOESTER FORMATION AND CATALYSIS OF SUBSTRATE UBIQUITINATION).  
FT MUTAGEN 777 777 C->A: LOSS OF UBIQUITINATION.  
SQ SEQUENCE 809 AA; 91816 MW; 6P183638447E70F CRC64;

Query Match 36-8%; Score 1484; DB 1; Length 809;  
Best Local Similarity 37.1%; Pred. No. 2, 6e-98;  
Matches 324; Conservative 125; Mismatches 224; Indels 200; Gaps 20;

QY 11 PYKLRITVCAKNLVKDKFFRLPDPFAKVVDPGSGQCHSTDYTVNTLDPKWNQHYDL-YI 69  
Db 2 PSISVCLVAEESLYKRDVRSPDPAVLTIDG-QTKRTSAAKTLNPKYNNFVKFDI 60

QY 70 GRKDSVTISWANHKKHKKGAGFICCVRL-LSNAINRLKD---TGYQR---LDLC 118  
Db 61 NEVSLITIQVEQQKF-KKXDGFLGVNVNRYGVDTGLHDEDATSSGRPREETITRDLK 119

QY 119 KLGSPNDIDTVRQIVV-----SLSRSRIGTGTQVWCSR--- 153  
Db 120 K-SNDGMASVGRLLIVVSKLPSSPHQSAPSGHTASSSTNTSSTRNGHTSSTRNHS 177

Db 154 -----LFDND---LPDGWB 165

Db 178 TSHPSRTQAQAVESTLOSSGTTAAATNTATTSHRSSTTSATRQSSFEQYGRIPPGHE 237

QY 166 RRTASGRTOYLNHHITRTTOWERPRTPASE-----YSSSPGRPLSCFVDENT 210  
Db 238 RTDNFGRTYYVDHNTRTTWKRPLTDQEAEGRQNANTELERQHRGRTLPGSSSDNS 297

QY 211 -----PISG-----TNGATGQSSDPLAERRVSQRIRNYMARTHLT 249

Db 298 SYTVQVGGSNIIPVNNGAAAAAAFAATGGTISGLG----- 331

QY 250 PPDLPEGTYQRTTQQGQVYFLHTQTGYSTWHDPYRVLDSMN-----CEBLGPL 299

Db 332 -ELPSGMQERFPEGRAYFDHNTRTTWMDPQRQOYTITYGPINTLQQQPSQLGPL 389

QY 300 PPGEWEIRNTATGPVIFVDHNRTQFTDPRLSANLHLVLRQNQLKDQQQVYSLCPDD 359

Db 390 PGSMEMRLNTARVYFDHNTKTWDPRPLSSL-----DQ----- 426

QY 360 TECIUTPVKPYKRDIVOKTILRQLSQQPO---AGCHRIVSRVSYQVMKRP 415

Db 427 ---NVPQVQRDRKRTKVIYFR---SQPALRILPQSOCHIKVRKNCNIPDAYQEMRQP 477

QY 416 KDLWKRMNTRKFRGEGLDYGGVAREWLYLISHEMLNPYGLFOYSRDDIYTLOQINPDSAV 475

Db 478 EDLKRMNTRKFDDEBGGYTSRBFFLUSHENMPFLFEAYDNTIQQNPNGI 537

QY 476 NPHELSYFHVGIMGMNAVFGHYYDGGPTLPPYFQLGKSIITLDDMELVDPDLHNSLVW 535

538 NPEHILNPFPIGRVYGLGFHRFLDAFFGALYKNNLRKCKVLQMEGIVDAEVNSLW 597	DR; GO:0004842; F:ubiquitin-protein ligase activity; IDA.
536 ILENDITGUDHPCVEANAYGELIQLHELPNGKSLEPNEENKEVNRILVNWRFLRGIE 595	DR; InterPro; IPR000008; C2.
598 MLENSDGVLDLIFASDDERFGEVVTDLKPDRNTEVTDGNKEYVELYTQKRVIDRVQ 657	DR; InterPro; IPR001202; WW_Rsp5_WWP.
596 AQPFLQKGNEVTPQHLLRTFDEKELELIICLGKIDVNDWKVNTRLKHCTPDNSVQH 655	DR; Pfam; PF00532; HECT_1.
658 EQPKRFLMDGENNLPEDLTVTFDERELLLIGIAEDIEDWKKHTDYGYQESDEVIQN 717	DR; SMART; SM00119; HECTC_1.
656 FWKAVEFFDEERRARLLOFTGSSRVPLOGFKAQAGAPRLFTIHQIDACTNNLPAKAT 715	DR; PROSITE; PS00495; C2 DOMAIN_1;
718 FWKCVSEWDNEQRARLLOFTGTSRIPVNGFKDQLGSDFPRFTERAGE-VQQLPSHT 776	DR; PROSITE; PS50004; C2_DOMAIN_2;
716 CENFDIPIPYESTEKLKYKLLTIAETGFAVE 748	DR; PROSITE; PS50237; HECT_1.
777 CFNRVDSLQXVDYDSMKQXLTLAVEETFGQE 809	DR; PROSITE; PS01154; WW_DOMAIN_1;
<b>SUJLT 7</b>	
NED4 MOUSE P46 <sup>75</sup> ; STANDARD; PRT; 957 AA.	KW; UBL conjugation pathway; Ligase; Repeat.
01-OCT-1995 (Rel. 32, Created) 15-SEP-2003 (Rel. 42, Last annotation update)	FT NON_TER 1 UBIQUITIN (BY SIMILARITY).
MUS musculus (Mouse). Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus . [1] REVISIONS. [2] REVISIONS.	FT DOMAIN 1 C2 DOMAIN.
Kumar S.; (MAY-1996) to the EMBL/GenBank/DBJ databases. -!- FUNCTION: E3 ubiquitin-protein ligase which accepts ubiquitin from -!- an E2 ubiquitin-conjugating enzyme in the form of a thioester and -!- then directly transfers the ubiquitin to targeted substrates (by -!- similarity).	FT DOMAIN 1 C2 DOMAIN.
-!- FUNCTION: INVOLVED IN THE EMBRYONIC DEVELOPMENT AND -!- TISSUE SPECIFICITY: BRAIN.	FT DOMAIN 1 C2 DOMAIN.
-!- MISCELLANOUS: A cysteine residue is required for ubiquitin- thioester formation.	FT DOMAIN 1 C2 domain.
-!- SIMILARITY: Contains 1 C2 domain.	FT DOMAIN 1 C2 domain.
-!- SIMILARITY: Contains 3 WW domains.	FT DOMAIN 1 C2 domain.
-!- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.	FT DOMAIN 1 C2 domain.
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BAA12803.1; -	DB; KKTQWEDPRL --- QNVATIGP --- AVP-YSDYKRYCEBFR 587
HSSP; Q13526; 1PIN.	DB; QELSOOOPQAGHCRIEVSREBIEFESYOMKNGPKDOLWK-RIMIKPRGEEGDLYGGVAR 439
MGD; MGI:972297; Nedd4.	DB; 588 RLRKQDIPNPKEMIPLRANILBPSYRR:MGYRADLKLKARUWIEFDGKGDDLYGGVAR 647
GO; GO:0000151; C:cytosol; IDA.	DB; 440 EMLYLSEHMNPYYGLFOYSRDIYTLQINPDSAV-NPEHLSYHFHYGRINGMAYPHGH 498
GO; GO:0005515; C:ubiquitin ligase complex; IPI.	DB; 648 EWFPLISKEMNPYGLFERSATINYTLQINPGLCNEDEHLSYKFGRVAGMAYHGK 707
GO; GO:0005515; F:protein binding activity; IPI.	DB; 499 YDGGFLPLFVKQULLKSILDDMELVDPDLANSLWILENDITGVLDTHTFCYHNGYE 558
GO; GO:0005515; F:protein binding activity; IPI.	DB; 708 LIDGFFTRPFYKMLQKLITLHDNESVYSSSLRWTILENDPT-ELDLRFITDEELFGQ 766

559	IQIELKLPGKSIIVNNEENKVEYRLTYNWRFRGIBAQFLAQKGFFNEVTPQHLLKTFD	6177
767	THQEELTGGSEBIVVTNCNKCEYIYLIVLQWRFNRICKOMAFAKEGFPELFPDLIKIFD	826
619	EKELELICGLGKIDNDWKVNTRLKH-CTPDSNIVKRMWKAFFDEERARLQLFVTG	677
827	ENEIELLINGLGDVDNDREHTKYKNGSYMHQVIWFWQAVMMDSERKIRLQLFVTG	886
678	SSRYVPLQGFKAQGAAGPRLFTIHQIDACTNNLPKAHTCFCNRIDPPYESEKLYKBLKT	737
887	TSRVPMPNGFAELYGSNGFOSFTYQW-GTPDKLPRAHTCFCNRIDPPYESFDELNDLQM	945
738	AIBETCGP	745
946	AIENTQGP	953
BUILT 8		
94	HUMAN NE4_HUMAN P44934;	STANDARD; PRT; 927 AA.
01	NOV-1995 01-NOV-1995 15-SEP-2003 NEPD4 OR KIAA0093	(Rel. 32, Created) (Rel. 32, Last sequence update) (Rel. 42, Last annotation update) NEPD4 protein (EC 6.3.2.-) (Fragment). Homo sapiens (Human). Mammalia; Eutheria; Chordata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Homo. NCBI_TaxID=9606;
SEQUENCE FROM N.A. TISSUE=Bone marrow; MEISSION=95308325; PubMed=7788527;		
Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S., Takata S., Ishikawa K.-I., Kawarabayasi Y., Kotani H., Nomura N.; "Prediction of the coding sequences of unidentified human genes. III. The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by analysis of cDNA clones from human cell line KG-1.", DNA Res. 1:37-43 (1995).		
-1 FUNCTION:E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATES (BY SIMILARITY)		
-1 MISCELLANEOUS: A cysteine residue is required for ubiquitin- thioester formation.		
-1 SIMILARITY: TO NEIL4 PROTEIN.		
-1 SIMILARITY: Contains 1 C2 domain.		
-1 SIMILARITY: Contains 4 WW domains.		
-1 SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.		
-----		
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-----		
EMBL: D42055; BAA07655; 1_P1N, HSSP: Q13526; 1_P1N, Genew: HGNC:727; NEDD4. MINI: 602278; -.		
InterPro: IPRO000008; C2; 1. InterPro: IPRO00569; HBCT_domain. InterPro: IPRO01202; WW_R3P5_WWP. PFAM: PF00158; C2; 1. PFAM: PF00632; HBCT; 1. PFAM: PF00397; WW; 4. PRINTS: PRO0360; C2DOMAIN. SMART: SM00329; C2; 1. SM00119; HBCT; 1.		

677	RLLDGEFFIREPFYKMLHKBPLHDMESYDSEYYNSLRWILENDPT-ELDRFLIDEELPG	735	Best Local Similarity 44.1%; Pred. No. 1.5e-37; Matches 135; Conservative 46; Mismatches 123; Indexes 2; Gaps 2;
558	EEIQBLKLNGKSIPVNEENKEEVRLVNRFLRGIEAQFLALQCFNEVTPQLIKTF	617	Qy 444 LLSHEMINPYTGFQYSRDIYTOINPDSAVNBEHLSVFHFVYGRIMAVTHGHYDGG 503
736	QTHQEKLNGGSETVVTNKGKEYIYLIVTQREVNRQKOMAAFKEGFFELIPQLIKIF	795	Db 2 IISRENEPNPYALFRTSIPLRVTSIHLPTVTTSSLAGRYVAKAVMTTALLECY 61
618	DEKEELLIITLGKGDVDWKVNTLKH-CTPPDSNVKVKWKAFFDEERARLLQFVT	676	Qy 504 FTLPLFYKQLLGSITLDDMELVDPDHSWILENDTATGVL-LHFTFCVEANAYGEITQH 562
796	DENEELLMCGLGHDVNDWREHTYKKGYSANHQVQWFWTAATMMDSEPRTRILQFVT	855	Db 62 PIRSFYKHLGSKSRYXTDMESEDHYFGVYVLLENDSTLGYLTPTSTEVQBFGVCEVR 121
677	GSSRVPLQGFKAAGAAGRPLFTHQIDACTTNLPLKAHTCFCNIDIPPYBSEYKLYEKL	736	Qy 563 ELKPNGKSIPTYNEENKEEYRFLYVWRFLRGIAQFLAQKGFEVTPQHLLKTFDEXEL 622
856	GTSR2DMNGFAELQSGNSQFSFTYEW-GTPERKLPAHTCENRLDLPPIESFEELWDKLQ	914	Db 122 DLRPANGANLIVTEENKEEYVHLVQMMRTGAIRKQLAAFLGFPFIIPLRLLTPEQEL 181
737	TAIEETCGF 745		Qy 623 EJTICGKGKIDYNDWKVNTTRLKHCTPSDNIVKWPKADEVDFERRARLQFTGSSVP 682
915	MAIENITQGP 923		Db 182 ELYTGGLPTIDDLSNTNEVKYQSNSTQIQWWFRALESFDQDRAKFLQFTVGTSKVP 241
SULT 9			Qy 683 LQGFKAQGAGAQPRLPFTHQIDACTTNLPLKAHTCENRLDIPPSYEEKLYEKTET 742
B1 RAT	STANDARD; PRT; 310 AA.		Db 242 LQFAALEGMMNIQKEQFQIHRDDRSTDRPSAHTCENQOLDPAYSFKLRRHMLLAIQEC 301
P51533;			Qy 743 C-CAFAV 747
01-OCT-1996	(Rel. 34, Created)		Db 302 SEQFGL 307
01-OCT-1996	(Rel. 34, Last sequence update)		
15-SEP-2003	(Rel. 42, Last annotation update)		
DNA binding protein URE-B1	(EC 6.3.2.-).		
UREB1.	Rattus norvegicus (Rat)		RESULT 10
Eukaryota; Mecozzo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butchia; Rodentia; Sciurognathi; Murinae; Rattus. NCBi_Taxid=10116;		UE3A_HUMAN STANDARD; PRT; 875 AA.	
[1]	SEQUENCE FROM N.A.	ID Q05086; P78155; Q93056; [1]	AC Q05086; P78155; Q93056; [1]
TISSUE=Brain;		DT 01-NOV-1997 (Rel. 35, Created)	
Gu J., Ren K., Dubner R., Iadarola M.J.;		DT 30-MAY-2000 (Rel. 39, Last sequence update)	
"Cloning of a DNA binding protein that is a tyrosine kinase substrate and recognizes an upstream initiator-like sequence in the promoter of the preprodynorphin gene,"		DT 15-SEP-2003 (Rel. 42, Last annotation update)	
Brain Res. Mol. Brain Res. 24:77-88 (1994).		DE Ubiquitin-protein ligase E3A (EC 6.3.2.-) (Oncogenic protein-associated protein E6-AP) (Human Papillomavirus E6-associated protein). DE Protein E6-AP OR E6AP.	
-!- FUNCTION: MAY BE A DNA-BINDING TRANSCRIPTIONAL REGULATOR.		GN Homo sapiens (Human).	
MEIDLINE=9058008; PubMed=7963380;		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Gu J., Ren K., Dubner R., Iadarola M.J.;		OC Mammalia; Butchia; Primates; Catarrhini; Hominidae; Homo.	
"Cloning of a DNA binding protein that is a tyrosine kinase substrate and recognizes an upstream initiator-like sequence in the promoter of the preprodynorphin gene."		NCBI_TaxID=9606;	
Brain Res. Mol. Brain Res. 24:77-88 (1994).		RN [1]	
-!- RECOGNIZES AN UPSTREAM INITIATOR-LIKE SEQUENCE IN THE PROMTER OF THE PREPRODYNORPHIN GENE.		RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.	
-!- AN E2' UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATES (BY SIMILARITY);		RC TISSUE=keratinocytes; MEDLINE=97288525; PubMed=9143503;	
-!- MISCELLANEOUS: A cysteine residue is required for ubiquitin-thiol ester formation. Contains 1 HECT-type E3 ubiquitin-protein ligase domain.		RX RA Yamamoto Y., Huilegote J.M., Howley P.M.; RT "The human E6-AP gene (UBB3A) encodes three potential protein isoforms generated by differential splicing." RT Genomics 41:263-266 (1997).	
-!- Similarity: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.		RL Mol. Cell. Biol. 13:775-784 (1993).	
EMBL; U08214; AAA81950.1; -.		RN [12]	
InterPro; IPR000569; HECT_domain.		RP SEQUENCE OF 11-875 FROM N.A., PARTIAL SEQUENCE, AND VARIANT VAL-290.	
pfam; PF00632; HECT; 1._		RC TISSUE=retinoblastoma; MEDLINE=3140775; PubMed=8380895;	
PROSITE; PS02037; HECT; 1.		RX RA Hubbrecht J.M., Scheffner M., Howley P.M.; RT "Cloning and expression of the cDNA for E6-AP, a protein that mediates the interaction of the human Papillomavirus E6 oncoprotein with p53"; RT Generated by differential splicing." RT Genomics 41:263-266 (1997).	
UbI conjugation Pathway; Ligase; Repeat; DNA-binding;		RL Mol. Cell. Biol. 13:775-784 (1993).	
Transcription regulation.		RN [13]	
DOMAIN 202 310 HECT.		RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT VAL-290.	
BINDING 275 275 UBIQUITIN:		RX MEDLINE=97141922; PubMed=8888172;	
SEQUENCE 310 AA; 35640 MW; D6E7F21FA70068E CRC64;		RA Matsura T., Sutcliffe J.S., Fang P., Galjaard R.-J., Jiang Y.-H., Benton C.S., Rommens J.M., Beaudet A.L.; RA	
Query Match	15.5%; Score 626; DB 1; Length 310;		

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EMBL; U08214; AAA81950.1; -.

InterPro; IPR000569; HECT\_domain.

pfam; PF00632; HECT; 1.\_

PROSITE; PS02037; HECT; 1.

UbI conjugation Pathway; Ligase; Repeat; DNA-binding;

Transcription regulation.

DOMAIN 202 310 HECT.

BINDING 275 275 UBIQUITIN:

SEQUENCE 310 AA; 35640 MW; D6E7F21FA70068E CRC64;

Query Match

"De novo truncating mutations in E6-AP ubiquitin-protein ligase gene (UBE3A) in Angelman syndrome.";  
Nat. Genet. 15:74-77(1997).  
[5]- VARIN AS ILE-826 TNS, AND VARIANT HIS-62; THR-201 AND PRO-372.  
MEDLINE=98234455; PubMed=9585605;  
Malzac P., Webber H., Monclia A., Graham J.M. Jr., Kukllich M.;  
Williams C., Pascon R.A., Ramsdell L.A., Kishino T., Wagstaff J.;  
"Mutation analysis of UBE3A in Angelman syndrome patients.";  
Am. J. Hum. Genet. 62:1353-1360(1998).  
CHARACTERIZATION:  
MEDLINE=9831563; PubMed=9688277;  
Noller U., Schwarz S.E., Scheffner M.;  
"The ubiquitin-protein ligase E6-associated protein (E6-AP) serves as  
its own substrate.";  
Bur. J. Biochem. 254:643-649(1998).  
-1- FUNCTION: INTERACTS WITH THE E6 PROTEIN OF THE CANCER-ASSOCIATED  
HUMAN PAPILLOMAVIRUS TYPES 16 AND 18. THE E6/E6-AP COMPLEX BINDS  
TO AND TARGETS THE P53 TUMOR-SUPPRESSOR PROTEIN FOR UBIQUITIN-  
MEDIATED PROTEOLYSIS. IT IS AN E3 UBIQUITIN-PROTEIN LIGASE WHICH  
ACCEPTS UBIQUITIN FROM AN E2 UBIQUITIN-CONJUGATING ENZYME IN THE  
FORM OF A THIOESTER AND THEN DIRECTLY TRANSFERS THE UBIQUITIN TO  
TARGETED SUBSTRATES. IT CAN TARGET ITSELF FOR UBIQUITINATION IN  
VITRO AND EFFICIENTLY PROMOTES ITS OWN DEGRADATION IN VIVO. IT  
APPEARS THAT ONLY UNMODIFIED E6-AP MOLECULES CAN BIND EFFICIENTLY  
TO P53 IN THE PRESENCE OF THE HSV E6 ONCOPROTEIN.  
-1- SUBCELLULAR LOCATION: Nuclear (Probable).  
-1- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=3;  
Name=III;  
IsoId=q05086-1; Sequence=Displayed;

Name=III;  
IsoId=q05086-2; Sequence=VS\_P\_006705;  
IsoId=q05086-3; Sequence=VS\_P\_006706;  
-1- DISEASE: DEFECTS IN UBE3A ARE A CAUSE OF ANGELMAN SYNDROME (AS),  
ALSO KNOWN AS 'HAPPY PUPPET SYNDROME'. IT IS CHARACTERIZED BY  
FEATURES OF SEVERE MOTOR AND INTELLECTUAL RETARDATION,  
MICROcephaly, ataxia, frequent jerky limb movements and flapping  
of the arms and hands, hypotonia, hyperactivity, hypopigmentation,  
seizures, absence of speech, frequent smiling and episodes of  
paroxysmal laughter, and an unusual facies characterized by  
macrostomia, a large mandible and open-mouthed expression, a great  
occipital groove, for protruding the tongue ('tongue thrusting'), and an  
occipital groove.  
-1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-  
THIOESTER FORMATION.  
-1- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase  
domain.  
-1- SIMILARITY: SOME, IN THE C-TERMINAL HALF, TO RAT 100 kDa PROTEIN.

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the European Bioinformatics Institute. There are no restrictions on its  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; L07557; AAA35542.1; ALT\_INIT.  
DR EMBL; AF016708; AAB69154.1; "-".  
DR EMBL; AF016703; AAB69154.1; JOINED.  
DR EMBL; AF016704; AAB69154.1; JOINED.  
DR EMBL; AF016705; AAB69154.1; JOINED.  
DR EMBL; AF016706; AAB69154.1; JOINED.  
DR EMBL; AF016707; AAB69154.1; JOINED.  
DR EMBL; U84404; AAB43301.1; "-".  
DR DDB; 1CAZ; 17-NOV-99.  
DR DDB; 1DSF; 17-NOV-99.  
DR DDB; 1EQX; 28-FEB-01.  
DR Genew; HGNC:12496; UBE3A.  
DR NMIM; 601632; "-".  
DR DR GO:0004840; Ubiquitin conjugating enzyme activity; TAS.  
DR GO:0007420; Protein development; TAS.  
DR GO:00061508; P: proteolysis and peptidolysis; TAS.  
DR InterPro; IPR000569; HECT\_domain.  
DR Pfam; PF00632; HECT; 1.  
DR SMART; SM00119; HECT; 1.  
DR PROSITE; PS50237; HECT; 1.  
DR Nuclear protein; ubi conjugation pathway; Ligase;  
KRN Alternative splicing; Disease mutation; Polymorphism; 3D-structure.  
FT DOMAIN 394 399 Disease mutation; ASP/GLU-RICH (ACIDIC).  
FT DOMAIN 776 875 HECT.  
FT BINDING 843 843 UBIQUITIN (BY SIMILARITY).  
FT VARSPLIC 1 23 Missing (in isoform 1).  
FT VARSPLIC 1 10 /FTID=VSP\_005705.  
FT VARSPLIC 1 10 MEKHOCWK --> MATACKR (in isoform III).  
FT VARIANT 44 44 /FTID=VSP\_006706.  
FT VARIANT 44 44 C --> Y (PROBLEMS POLYMORPHISM).  
FT VARIANT 62 62 /FTID=VAR\_007852.  
FT VARIANT 201 201 R --> H.  
FT VARIANT 201 201 /FTID=VAR\_00142.  
FT VARIANT 290 290 A --> T.  
FT VARIANT 290 290 /FTID=VAR\_007853.  
FT VARIANT 372 372 G --> V.  
FT VARIANT 826 826 P --> V.  
FT VARIANT 826 826 /FTID=VAR\_008144.  
FT CONFLICT 359 359 R --> R (IN REF. 2).  
FT CONFLICT 423 423 P --> L (IN REF. 2).  
FT CONFLICT 647 649 TFR --> LFV (IN REF. 2).  
FT CONFLICT 669 669 E --> V (IN REF. 2).  
FT CONFLICT 686 686 D --> N (IN REF. 2).  
SQ SEQUENCE 875 AA; 100645 MW; 667925F1956670AA CRC64;  
SQ SEQUENCE 875 AA; 100645 MW; 667925F1956670AA CRC64;

Query Match Score 539; DB 1; Length 875;  
Best Local Similarity 13.3%; Score 539; DB 1; Length 875;  
Matches 183; Conservative 117; Mismatches 277; Indels 152; Gaps 22;

Qy 105 NFKLDTYQRDLCKPGN---DNDFVQGVVLSQSDRIGG----GQVQDCS 152  
Dd 212 SRIGDSSQGDNNLQLGPDDVSDIDAIR-RVYTRLLSNEKIAFLNALVYSPNVECD 270  
Qy 153 RLFDNDLPGWERRATASGRIQYLHHTTTQWPRPRAEYSSGPRPLSCVDENTPI 212  
Dd 271 LYHN-----VYSRDPNYLNLF--LIGMENRNLHSPEVLEMAPLFCAMSKLPL 318  
Qy 213 SGT-----NGATCQSSDPLARRR----232  
Dd 319 AQGKLTRLWKNYNAQIRNMNETFQQLTYKVSNFNSRNLYNDDAIVASKCLKRMV 378  
Qy 233 ---VRSQRHRYNMSRTHLHTPPDLPE---GYFORTQOGOYVFLHTQTGVSTWH 280  
Dd 379 YYANVVGGEVTDNHNEEDDEBPIPSESSLTQELIGEERRKKGPRVDPLTLGVK---436  
Qy 281 DPRVPRLSINCBELGJPLPGWEFRNTATGRV-----YFYDHNNRTQFTDPL- 330  
Dd 437 -----LDCRK--PLTFPEETFNEPLNEVLEMDKDYTFKVEVENKFSSMTCPSTL 484

331 -SANLHLVNRNQNLKDQQQQVVSICPDDTECLTVPRYKRDLVQKLKTLRQLBSQQQPQ 389  
 485 NAVTQNLGKYDNRIMYSTERITYL-----YSVQSQL 519  
 390 AGHCRIEVSREPIFEE--YRQVMGRMPKDILWKLMLKFRGEGLDYGVAEBWLYLIS 446  
 520 NEPLRLKVRDRHTIDALVLREMINAMENPADLKKGQLYVEFEGEQVDEGGVSKSEFFQLVV 579  
 447 HEMLNPNYGLFQYSDIYTQINPDSAVNPEHLSYFHVGRRINGMAYFHGHYIDGFTL 506  
 580 EBIINPDIGMFTD-ESTKLFWNSSF--ETEQQFLIGIVLGNCLDVFPPM 635  
 507 PYKQKLIGKSITLDLNEELVDPDLNSLWVL--ENDITGFLDHTFCV-EHNAYGEILOHE 563  
 636 VTYRKLGKKGKTFRDGDSPVLYSLDPLVYDNEEDDMMTFQISQTDLFGNPMDY 695  
 564 LKPNGKSTIPVNEENKKYVRLYVNVWRFLRGTEAOPFLAQKGFNEVIPQHLLK-TDEKEI 622  
 696 LKENGDKIPNTNENKFVNLYSDITLANKSVEKQKAFLRGRFMNTVESPLAKYLRBEEI 755  
 623 ELIJICLGKPKDWNDCYNTRLK-HCTPDSNIVKRNWKAVEFFDEERRRLQFTVSSRV 681  
 756 ELLICGGRNLDFQALEBETTYDG37RDSTVLFREWEIHTSFDEQRKLFLQFTTGIDRA 815  
 682 P1QG--FKAQGAASPRLFIHQDACTINNLPRHTCPNRIDPYESYKLYEKULTA 738  
 816 PVGGLGKLMKIAKNPD-----TERLPISHTCNVJLIPYEYSSKEKIKERLIIKA 865  
 739 IETTCGPAV 747  
 866 ITYAKGFGM 874  
 SULT 1.1  
 3'UE3\_MOUSE STANDARD; PRT; 885 AA.  
 Q08759; P97482; 30-MAY-2000 (Rel. 39, Created)  
 28-FEB-2003 (Rel. 41, Last annotation update)  
 Ubiquitin-protein ligase E3A (EC 6.3.2.-) (Oncogenic protein-associated protein E6-AP).  
 Mus musculus (Mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID:10090;  
 SEQUENCE FROM N.A.  
 STRAIN-C57BL/6 X CBA;  
 MEDLINE=971226076; PubMed=9182527;  
 Hatayama S., Jensen J.P., Weissman A.M.;  
 "The E6-AP ubiquitin-protein ligase (UBE3A) gene is localized within interactions of mammalian and ubiquitin-conjugating enzyme (E2B) interactions from N.A.";  
 J. Biol. Chem. 272:15085-15092 (1997).  
 SEQUENCE FROM N.A.  
 STRAIN-BALB/c; TISSUE=Brain;  
 MEDLINE=9726434; PubMed=110176;  
 Sutcliffe J.S., Jiang Y.-H., Galjaard R.-J., Matsunaga T., Fang P., Beaudet A.L., Bressler J., Cattanach B., Ledbetter D.H., "The E6-AP ubiquitin-protein ligase WHICH ACCEPTS UBIQUITIN FROM a narrowed Angelman syndrome critical region.";  
 Genome Res. 7:1368-1377(1997).  
 -1- FUNCTION: E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM AN E2 UBIQUITIN-CONjugating ENZYME IN THE FORM OF A THIOESTER AND THEN DIRECTLY CONFERGES THE UBIQUITIN TO TARGETED SUBSTRATES.  
 -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.  
 -1- TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, HEART AND THYMUS.  
 -1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-THIOLESTER FORMATION.  
 -1- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase

domain. domain. domain.  
 -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-38 IS THE INITIATOR.  
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 CC  
 EMBL; U96636; AAB63361; -.  
 DR EMBL; U87122; AAB677561; -.  
 DR MGD; MGT:1.05098; Ube3a.  
 GO; GO:0005839; C:cytosol; IDA.  
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 GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.  
 InterPro; IPI000669; HECT\_domain.  
 Pfam; PF00632; HECT\_1.  
 SMART; SR00111; HECT\_1.  
 DR PROSITE; PS05037; HECT\_1.  
 KW Nuclear protein; UbI conjugation pathway; Ligase.  
 FT DOMAIN 405  
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 FT DOMAIN 405  
 DOMAIN 405  
 DR GO; GO:0005634; C:nucleus; IDA.  
 DR GO; GO:0005515; F:protein binding activity; IPI.  
 DR InterPro; IPI000669; HECT\_domain.  
 SMART; SR00111; HECT\_1.  
 DR PROSITE; PS05037; HECT\_1.  
 KW Nuclear protein; UbI conjugation pathway; Ligase.  
 FT DOMAIN 405  
 DOMAIN 405  
 DR GO; GO:0005634; C:nucleus; IDA.  
 DR GO; GO:0005515; F:protein binding activity; IPI.  
 DR InterPro; IPI000669; HECT\_domain.  
 SMART; SR00111; HECT\_1.  
 DR PROSITE; PS05037; HECT\_1.  
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 DR GO; GO:0005515; F:protein binding activity; IPI.  
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 DR GO; GO:0005515; F:protein binding activity; IPI.  
 DR InterPro; IPI000669; HECT\_domain.  
 SMART; SR00111; HECT\_1.  
 DR PROSITE; PS05037; HECT\_1.  
 KW Nuclear protein; UbI conjugation pathway; Ligase.  
 FT DOMAIN 405  
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 DR GO; GO:0005634; C:nucleus; IDA.  
 DR GO; GO:0005515; F:protein binding activity; IPI.  
 DR InterPro; IPI000669; HECT\_domain.  
 SMART; SR001

523	SLVQGQINPNTITLKVRRDHLIDDLALVRLEMIAAMENPADLKQKLVYVEFEGQYDEGGVS	582
439	REWLYLISHMNPYGLFOYSRDIYTL-QINPDSAVNPEHLSYFHFYGRIMMAVPHG 497	
583	KFFFLQVVEEFNPDIGMTY -DEATKLFWNFNPSSF-- ETEGGFTLIGLAIVNN 636	
498	HYDGGTLPFKQKLLGSITDDMLLVDPLAHSWILEND-----ITGVLDHTF 549	
637	CILDVHPMPVYVKLMMKKGKPTFDLGDSPHPVLYQOSLKDLEYEQQSVEDDNMMITFQISCF- 695	
550	CVEHNAAGEIIQHELXNGKSIPVNBEENKCEYVRLVNVWRFLRGIEAQFLALQKFNEVYI 609	
696	--DLGNPNMMDLKENGDKIPITENRKEFVISYSDYLLNKSTEKOPFAERGGPHMYT 751	
610	POHLKL-TFDEKEBLJLICLGKIDYNDWKYNTLRK-HCTPDNSVTKWFWKAVEFDFEER 667	
752	NESPPLKYLFRPEELICLIGSRNLDFQALEETTEDGGTGTRESVVTFREFEVIVSFTDQ 811	
668	RARLLOCFTGSSRVPLQG--PKALQGAAGRFLFTHQIACTNNLPKAHTCFCNRIDIPP 724	
612	KLFLLFLTGTDPRPVEGLKURMIAKNGPD-----TERPLTSHTCFNVLILPS 861	
725	YESYEKLYEKLTIAETTCGFAY 747	
862	YSSKEKLUNVRLKAITYAKGFM 884	
WULF 112		
4 YEAST		
H014 YEAST		
P=0.985;		
01-FEB-1995 (Rel. 31, Created)		
01-NOV-1995 (Rel. 32, Last sequence update)		
28-FEB-2003 (Rel. 41, Last annotation update)		
Probable ubiquitin- <sup>a</sup> proteine ligase HUL4 (EC 6.3.2.-):		
HUL4 OR YJR036C OR J4608.		
Bakaryo, Fungi; Ascomycota; Saccharomycotina; Saccharomyces; Saccharomycetales; Sacccharomycetaceae; Sacccharomyces.		
NCBI_TaxID=1932;		
[1]		
SEQUENCE FROM N.A.		
STRAINS288C.		
MEDLINE-953971595; PubMed=7668047;		
Huang N.-E., Chuat J.-C., Galibert F.: "Analysis of a 42.5 kb DNA sequence of chromosome X reveals three tRNA genes and 14 new open reading frames including a gene most probably belonging to the family of ubiquitin-protein ligases."; Yeast 11:775-781(1995).		
[2]		
SEQUENCE OF 362-892 FROM N.A.		
MEDLINE-95049431; PubMed=7957102;		
van Gool A.J., Vethage R., Swartakers S.M.A., van de Putte P., Brouwer J., Troelstra C., Bootma D., Hoijmakers J.H.J.; "The functional S. cereviciae homolog of the Cockayne syndrome B gene ERCC6"; EMBO J. 13:5561-5569 (1994).		
[3]		
GENE NAME, AND GENE DISRUPTION.		
MEDLINE-9071972; PubMed=9838556;		
Wang G., Yang J.J., Huibregtsse J.M.;"Functional domains of the rps5 ubiquitin-protein ligase.";		
MO. Cell. Biol. 19:312-312 (1999).		
-1- FUNCTION: PROTEASE E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM AN E2 UBIQUITIN-CONjugating ENZYME IN THE FORM OF A THIOESTER, AND THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATES. NON ESSENTIAL.		
-1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-THIOESTER FORMATION (BY SIMILARITY)		
-1- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain		

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643 LRHCTDDSNIVRWFRAVERDEERARLIQFVTGSSRVPLQQFKALQGAAGPRLFTIHQ 702  
 793 VGGFEDDSRAVCWFEEWDFYIPIQKLTQVTAASDRPATISTPPKIS-.JLGSHD 850  
 703 IDACTNNPLKAHTCNRIDIPPEYEYKLEYKLTIAETTCGF 745  
 851 SD---DLPLAHTCNEICLWNYYSSKKKELKLWAINESEGY 889

SULT 13  
 R3\_HUMAN STANDARD; PRT; 1050 AA.  
 Q15034; (Rel. 35, Created)  
 01-NOV-1997 (Rel. 35, Last sequence update)  
 28-FEB-2003 (Rel. 41, Last annotation update)  
 HERC3 domain and RCC1-like domain Protein 3.  
 HERC3 OR KIAA0042.  
 Homo sapiens (Human).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Butcheria; Primates; Catarrhini; Hominidae; Homo;  
 NCB\_ Taxid=9606;  
 [1] SEQUENCE FROM N.A.  
 TIS-B=Bone marrow; MEDLINE=960511387; PubMed=7584026;  
 Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Y.,  
 Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;  
 "Prediction of the coding sequences of unidentified human genes. I.  
 The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by  
 analysis of randomly sampled cDNA clones from human immature myeloid  
 cell line KG-1.", DNA Res. 1:27-35(1994).  
 [2] CHARACTERIZATION.  
 MEDLINE=21099818; PubMed=11163799; Rosa J.L.;  
 Cruz C., Ventura F., Barrion R., Rosa J.L.;  
 "HERC3 binding to and regulation by ubiquitin.", FEBS Lett. 488:74-80(2001).  
 -1- SUBCELLULAR LOCATION: Cytoplasmic. Also found in vesicular-like  
 structures.  
 -1- PTM: Substrate of ubiquitination and is degraded by the  
 proteasome.  
 -1- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase  
 domain.  
 -1- SIMILARITY: Contains 7 RCC1 repeats.

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EMBL; D25215; BAA04945.1; -.  
 GeneID: HGNC:4876; HERC3; -.  
 NM\_00119; RCC1.1.  
 NM\_00200; -.  
 PROSITE; PS00237; HECT; 1.  
 InterPro; IPR000408; Reg\_Chr\_condens.  
 Pfam; PF00632; HECT; 1.  
 PRINTS; PR00633; RCCNDNSATION.  
 SMART; SM00119; RCC1.1.  
 PROSITE; PS00625; RCC1.1; FALSE\_NEG.  
 PROSITE; PS00626; RCC1.2; 4.  
 PROSITE; PS00102; RCC1.3; 7.  
 UBL conjugation pathway; Ubl conjugation; Repeat.  
 REPEAT 1 51 RCC1.1.  
 REPEAT 1 101 RCC1.2.  
 REPEAT 1 154 RCC1.3.  
 REPEAT 1 207 RCC1.4.

FT REPEAT 208 259 RCC1.5.  
 FT REPEAT 261 311 RCC1.6.  
 FT DOMAIN 213 366 RCC1.  
 FT BINDING 951 1050 HECT.  
 SQ SEQUENCE 1018 1018 UBIQUITIN (BY SIMILARITY).  
 SQ SEQUENCE 1050 AA; 117188 MW; SF0BALDEF40B912 CRC64;  
 Query Match 11.0%; Score 445.5; DB 1; Length 1050;  
 Best Local Similarity 31.6%; Pred. No. 6; 9e-24; Gaps 9;  
 Matches 115; Conservative 69; Mismatches 151; Indels 29; Gaps 9;  
 Qy 395 IEYSREEFEESEYROYKMRPKDLYFLRMLIKFRREGLDYGGVAREMLYLHSHEMLNPY 454;  
 Db 704 LH|YRRNNLVGDALRELTSIHDLLRPLKVIFDGBEAVDGTVTFULLKBSLNPY 763  
 Qy 455 GLFQYSRDIIYTLQINDSAVNPEHLSYFFHVGIRGMGVFHGAYIDGFTLPPYKQLG 514  
 Db 764 GMTTYYQQS--NLLWFEDTCF\_VEH\_NWFHJIGITGGLATYNSTVVDLFLPLAYKQLLN 819  
 Qy 515 KSTITLDDMLVDDDLANSLWVILENDITGV-LDHTFCVE ---ANAYGEFLICHLKPNKG 569  
 Db 820 VKPSELQDLEKSLTEGRSLOELL--DYPGEDEVEETFLANTICESYGVIEQKLIPGGD 877  
 Qy 570 SIPPYNEENKEKTYRLYNNWRFLRGIBAQFLNLQKGGENVPQHILKTDFDEKELELLIGL 629  
 Db 878 NYTVCKKONRQEFPDAYNNYVQISHEWYTAFASSFLKVGKVLBFQPSELFAMMVEN 937  
 Qy 630 GKDVND----WKNTRLRLKTPDSNIVKWFVAEFTDEERARLQFTVTESSRVL 683  
 Db 938 SNTYWEELEETAIKYKDYSATHP ---VKLWFETFHPEPLEKKKELFLTGSDRPI 992  
 Qy 684 QGPXALOGAGAPPLFTTHOIDACTNNPLKAHTCFNRIDIPPEYESYKLYEKLLTAIEETC 743  
 Db 993 YGMASLQ-----IVIQSTASGGEEYLPAVATCINLDPKSSREBLSARLQTQALDNE 1045  
 RESULT 14  
 TRIB\_HUMAN STANDARD; PRT; 1992 AA.  
 ID TRIB\_HUMAN STANDARD; PRT; 1992 AA.  
 AC Q14669; Q15644;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Thyroid receptor interacting protein 12 (TRIP12).  
 GN TRIP12 OR KIAA0045.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Chordata; Chordata; Vertebrata; Butelostomii;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=bone marrow;  
 RX MEDLINE=96051398; PubMed=7584044;  
 RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,  
 RA Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.;  
 RA "Prediction of the coding sequences of unidentified human genes. II.  
 RT The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by  
 RT analysis of cDNA clones from human cell line KG-1.";  
 RL DNA Res. 1:223-229(1994).  
 RN [2]  
 RP SEQUENCE OF 1801-1992 FROM N.A.  
 RX MEDLINE=55295737; PubMed=776974;  
 RA Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.;  
 RA "Two classes of Proteins dependent on either the presence or absence  
 RT of thyroid hormone for interaction with the thyroid hormone  
 receptor.", Mol. Endocrinol. 9:242-254 (1995).  
 CC FUNCTION: Component of PA700, an ATP-dependent multisubunit  
 -!- PROTEIN THAT ACTIVATES THE PROTEOLYTIC ACTIVITIES OF THE

MULTIFUNCTIONAL PROTEINASE (20S PROTEASOME) OF THE 26S COMPLEX. SPECIFICALLY INTERACTS WITH THE LIGAND BINDING DOMAIN OF THE THYROID HORMONE RECEPTOR (IN A THYROID HORMONE T3 INDEPENDENT MANNER) AND WITH RETINOID X RECEPTOR (RXR). COULD BE E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM AN E2 UBIQUITIN-CONJUGATING ENZYME IN THE FORM OF A THIOESTER AND THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATS.

-1 - SUBUNIT: IS 100% COMPOSED OF AT LEAST 16 DISTINCT PEPTIDES RANGING IN MOL. WT. FROM 20-112 kDa.

-1 - MISCELLANEOUS: A cysteine residue is required for ubiquitin-thioester formation.

-1 - SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.

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EMBL; D28476; BAA05837; 1; -. EMBL; I40383; AAC41731; 1; -. EMBL; I40383; AAC41731; 1; -. NMIM; 604506; -. GO; GO-0016523; F:ligand-dependent thyroid hormone receptor i. . . ; IDA. GO; GO-0014842; F:ubiquitin ligase activity; NAS. GO; GO-0016567; P:protein ubiquitination; NAS. InterPro; IPR000069; HECT domain. InterPro; IPR001170; WEE\_3om. Pfam; PF00632; HECT; 1. Pfam; PF02825; WHE; 1. SMART; SM00119; HECT; 1. PROSITE; PS0237; HECT; 1. Proteasome; Ubl conjugation pathway; Ligase.

DOMAIN 1885 1992 UBIQUITIN (BY SIMILARITY) :> QALRYA (IN

BINDING 1959 1959 SSIEFMREKULLIAAREGQOSFHLs -> QALRYA (IN

CONFlict 1969 1992 REF. 2)

SEQUENCE 1992 AA; 220332 MW; 29470C63A332DE CRC64;

Query Match 10 0% Score 404; DB 1; Length 1992; Best Local Similarity 25.5%; Pred. No. 1.6e-20; Matches 172; Conservative 91; Mismatches 218; Indels 194; Gaps 33;

180 TRT-TOWERPFPASESSSPRPLSCEVDNTPIGTNG--ATCGQSSDPRLAERRRSQ 236

> 1391 TKTHTIVYKPYREDEEESNK----DC-----VGGKRGRACQAPTKTSPRVNAKK---- 1433

> 237 RHNRYMSRTHLTHTPDLPDPEGYBQRITQQGVYTFITQEVSTWHD P-----RVRDRL 288

> 1434 ----HDELWHDGVCPVSNPLE-----VYLITPPENITFEDSDLVILLRLVHAI 1481

> 289 S-----NINCEELGPLPGWEIRNTATGRVYTFDPRLSANLHYLNR 340

> 1482 SRYWWYLYDNAMCKE1IP-----TSEFINSLKTAKAN---- 1513

> 341 QHQQLKD-----QQQQYVVSICP-----DDBCQL-TVPRTRKD-LVQKUKLRLQEL 383

> 1514 -RQDPLVMTGNIPITWLTEIGKTCPPFFPDITQMLPVTAIDRDAMQRLLDTPEI 1572

> 384 SQQQ-----POAGHCRIEVSREELFEESYRQWIKMRPKDLN-KRLMKPGEGLDYG 435

> 1573 NQDSQDRVARLDRKRTYNEBEEKQKQ-ESTM-----QDLGSSTRAMLEIQYENEVGTG 1627

> 436 -GYAREMYLLSHEMNPYGLFOYSRSDDTYTLQNPDA----- 474

> 1628 LGPTLEFYALQSQRADLGW---RGEBVTLNSNPKSSQEQTGYQIONQGLFALPFR 1683

> 475 -VREPHIS----YFHFGGRINGMAYFHGTYDGGTLPFKOLIGK---SITLDDMBLIVDP 527

> 1684 TAKPAHTAKVVKRERFLGKLMAKADMFLVLPLGLPFYKOMLRQETSLSLTHDLDIDP 1743

Qy 528 DLHNSLVW-----LEN-----ITGV-----	Db 1744 VVARVYHIEDIVRQKCRLEODQSQTKESSLQTALETITMNGCSVEDGLDTFLPGFPNI -	Db 1803 557 GEIIQHELKPNGKSIPIUNENKEVYRLYNNWRPLRGEAQFLALQKGNEVTPQHLLKT 616
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